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(54) Title: OB FUSION PROTEIN COMPOSITIONS AND METHODS

## (57) Abstract

The present invention relates to Fc-OB fusion protein compositions, methods of preparation of such compositions and uses thereof. In particular, the present invention relates to a genetic or chemical fusion protein comprising the Fc immunoglobulin region, derivative or analog fused to the N-terminal portion of the OB protein, derivative or analog.

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## OB FUSION PROTEIN COMPOSITIONS AND METHODS

Field of the Invention

5           The present invention relates to Fc-OB fusion protein compositions and methods for preparation and use thereof.

Background

10          Although the molecular basis for obesity is largely unknown, the identification of the "OB gene" and protein encoded ("OB protein" or "leptin") has shed some light on mechanisms the body uses to regulate body fat deposition. See, PCT publication, WO 96/05309  
15          (12/22/96), Friedman et al.; Zhang et al., Nature 372: 425-432 (1994); see also, the Correction at Nature 374: 479 (1995). The OB protein is active in vivo in both ob/ob mutant mice (mice obese due to a defect in the production of the OB gene product) as well as in normal, 20 wild type mice. The biological activity manifests itself in, among other things, weight loss. See generally, Barrinaga, "Obese" Protein Slims Mice, Science 269: 475-456 (1995). The OB protein, derivatives and use thereof as modulators for the 25 control of weight and adiposity of animals, including mammals and humans, has been disclosed in greater detail in PCT publication WO 96/05309 (12/22/96), hereby incorporated by reference, including figures.

30          The other biological effects of OB protein are not well characterized. It is known, for instance, that in ob/ob mutant mice, administration of OB protein results in a decrease in serum insulin levels, and serum glucose levels. It is also known that administration of OB protein results in a decrease in body fat. This was 35 observed in both ob/ob mutant mice, as well as non-obese normal mice. Pelleymounter et al., Science 269: 540-543

(1995); Halaas et al., Science 269: 543-546 (1995). See also, Campfield et al., Science 269: 546-549 (1995) (Peripheral and central administration of microgram doses of OB protein reduced food intake and body weight of *ob/ob* and diet-induced obese mice but not in *db/db* obese mice.) In none of these reports have toxicity's been observed, even at the highest doses.

Despite the promise of clinical application of the OB protein, the mode of action of the OB protein in vivo is not clearly elucidated. Information on the OB receptor, shows high affinity binding of the OB protein detected in the rat hypothalamus, which indicates OB receptor location. Stephens et al., Nature 377: 530-532. The *db/db* mouse displays the identical phenotype as the *ob/ob* mouse, i.e., extreme obesity and Type II diabetes; this phenotype is thought to be due to a defective OB receptor, particularly since *db/db* mice fail to respond to OB protein administration. See Stephens et al., supra.

With the advances in recombinant DNA technologies, the availability of recombinant proteins for therapeutic use has engendered advances in protein formulation and chemical modification. One goal of such modification is protein protection and decreased degradation. Fusion proteins and chemical attachment may effectively block a proteolytic enzyme from physical contact with the protein backbone itself, and thus prevent degradation. Additional advantages include, under certain circumstances, increasing the stability, circulation time, and the biological activity of the therapeutic protein. A review article describing protein modification and fusion proteins is Francis,

*Focus on Growth Factors* 3:4-10 (May 1992) (published by Mediscript, Mountview Court, Friern Barnet Lane, London N20, OLD, UK).

One such modification is the use of the Fc 5 region of immunoglobulins. Antibodies comprise two functionally independent parts, a variable domain known as "Fab", which binds antigen, and a constant domain, known as "Fc" which provides the link to effector functions such as complement or phagocytic cells. The 10 Fc portion of an immunoglobulin has a long plasma half-life, whereas the Fab is short-lived. Capon, et al., *Nature* 337: 525-531 (1989).

Therapeutic protein products have been constructed using the Fc domain to provide longer half-life or to incorporate functions such as Fc receptor binding, protein A binding, complement fixation and placental transfer which all reside in the Fc proteins of immunoglobulins. *Id.* For example, the Fc region of an IgG1 antibody has been fused to the N-terminal end of 20 CD30-L, a molecule which binds CD30 receptors expressed on Hodgkin's Disease tumor cells, anaplastic lymphoma cells, T-cell leukemia cells and other malignant cell types. See, U.S. Patent No. 5,480,981. IL-10, an anti-inflammatory and antirejection agent has been fused to murine Fc $\gamma$ 2a in order to increase the cytokine's short 25 circulating half-life. Zheng, X. et al., *The Journal of Immunology*, 154: 5590-5600 (1995). Studies have also evaluated the use of tumor necrosis factor receptor linked with the Fc protein of human IgG1 to treat patients with septic shock. Fisher, C. et al., *N. Engl. J. Med.*, 334: 1697-1702 (1996); Van Zee, K. et al., *The Journal of Immunology*, 156: 2221-2230 (1996). Fc has 30 also been fused with CD4 receptor to produce a therapeutic protein for treatment of AIDS. See, Capon et al., *Nature*, 337:525-531 (1989). In addition, the 35 N-terminus of interleukin 2 has also been fused to the

Fc portion of IgG1 or IgG3 to overcome the short half life of interleukin 2 and its systemic toxicity. See, Harvill et al., Immunotechnology, 1: 95-105 (1995).

Due to the identification of the OB protein as  
5 a promising therapeutic protein, there exists a need to develop OB analog compositions for clinical application in conjunction with or in place of OB protein administration. Such development would include OB analog compositions where protein formulations and  
10 chemical modifications achieve decreased protein degradation, increased stability and circulation time. The present invention provides such compositions.

Summary of the Invention

15 The present invention relates to Fc-OB fusion protein compositions, methods of preparation of such compositions and uses thereof. In particular, the present invention relates to a genetic fusion protein comprising the Fc region or analogs of immunoglobulins fused to the N-terminal portion of the OB protein or  
20 analogs. The Fc-OB fusion protein is capable of dimerizing via the cysteine residues of the Fc region. Unexpectedly, genetic fusion modification with Fc at the N-terminus of the OB protein demonstrates advantages in  
25 stability, clearance rate and decreased degradation which are not seen in OB protein or with fusion of Fc to the C-terminus of the OB protein. Surprisingly and importantly, the N-terminus modification provides unexpected protein protection from degradation,  
30 increases circulation time and stability, when compared to the OB protein or Fc modification to the OB protein C-terminus. Such unexpected advantages from the Fc modification to OB protein would be advantageous to OB protein consumers, in that these changes contribute to  
35 lower doses required or less frequent dosing. Thus, as described below in more detail, the present invention

has a number of aspects relating to the genetic modification of proteins via fusion of the Fc region to the OB protein (or analogs thereof), as well as, specific modifications, preparations and methods of use  
5 thereof.

Accordingly, in one aspect, the present invention provides a Fc-OB fusion protein wherein Fc is genetically fused to the N-terminus of the OB protein (or analogs thereof). In addition, the Fc portion may  
10 also be linked to the N-terminus of the OB protein (or analogs thereof) via peptide or chemical linkers as known in the art. As noted above and described in more detail below, the Fc-OB fusion protein has unexpected protections from degradation and increased circulation  
15 time and stability when compared to the OB protein or C-terminus OB-Fc fusion proteins. Additional aspects of the present invention, therefore, include not only Fc-OB fusion protein compositions, but also DNA sequences encoding such proteins, related vectors and host cells  
20 containing such vectors, both useful for producing fusion proteins of the present invention.

In a second aspect, the present invention provides for preparing the Fc-OB fusion protein. Such methods include recombinant DNA techniques for  
25 preparation of recombinant proteins. Furthermore, such aspects include methods of fermentation and purification as well.

In another aspect, the present invention provides methods for treating excess weight in an  
30 individual or animals, including modulation of and/or fat deposition by the administration of Fc-OB fusion proteins. Due to the Fc-OB fusion protein characteristics, methods are contemplated which reduce the amount and/or frequency of dosage of OB protein by  
35 using Fc-OB weight reducing agent.

In yet another aspect, the present invention provides for therapies for the treatment of co-morbidities associated with excess fat, such as diabetes, dys- or hyperlipidemias, arterial sclerosis, 5 arterial plaque, the reduction or prevention of gall stones formation, stroke, and also an increase in insulin sensitivity and/or an increase in lean tissue mass.

In another aspect, the present invention also provides for related pharmaceutical compositions of the 10 Fc-OB proteins, analogs and derivatives thereof, for use in the above therapies.

Brief Description of the Drawings

FIGURE 1 Recombinant murine metOB (double stranded) DNA (SEQ. ID. NOs.: 1 and 2) and amino acid sequence (SEQ. ID. NO. 3).

FIGURE 2 Recombinant human metOB analog (double stranded) DNA (SEQ. ID. NOs.: 4 and 5) and amino acid sequence (SEQ. ID. NO. 6).

FIGURE 3 (A-C) Recombinant human metFc-OB (double stranded) DNA (SEQ. ID. NOs.: 7 and 8) and amino acid sequence (SEQ. ID. NO. 9).

FIGURE 4 (A-C) Recombinant human metFc-OB variant (double stranded) DNA (SEQ. ID. NOs.: 10 and 11) and amino acid sequence (SEQ. ID. NO. 12).

FIGURE 5 (A-C) Recombinant human metFc-OB variant (double stranded) DNA (SEQ. ID. NOs.: 13 and 14) and amino acid sequence (SEQ. ID. NO. 15).

FIGURE 6 (A-C) Recombinant human metFc-OB variant (double stranded) DNA (SEQ. ID. NOs.: 16 and 17) and amino acid sequence (SEQ. ID. NO. 18).

Detailed Description

The present invention relates to Fc-OB fusion 35 protein compositions, methods of preparation of such compositions and uses thereof. In particular, the

present invention relates to the genetic or chemical fusion of the Fc region of immunoglobulins to the N-terminal portion of the OB protein. Unexpectedly, fusion of Fc at the N-terminus of the OB protein 5 demonstrates advantages which are not seen in OB protein or with fusion of Fc at the C-terminus of the OB protein. Surprisingly, the N-terminally modified Fc-OB protein provides unexpected protein protection from degradation, increased circulation time and increased 10 stability. Accordingly, the Fc-OB fusion protein, and analogs or derivatives thereof, as well as, related methods of use and preparation, are described in more detail below.

15                   Compositions

The Fc sequence of the recombinant human Fc-OB sequence set forth in SEQ. ID. NO. 9 (See Figure 3) may be selected from the human immunoglobulin IgG-1 heavy chain, see Ellison, J.W. et al., Nucleic Acids Res. 10: 20 4071-4079 (1982), or any other Fc sequence known in the art (e.g. other IgG classes including but not limited to IgG-2, IgG-3 and IgG-4, or other immunoglobulins). Variant, analogs or derivatives of the Fc portion may be constructed by, for example, making various 25 substitutions of residues or sequences.

Cysteine residues can be deleted or replaced with other amino acids to prevent formation of disulfide crosslinks of the Fc sequences. In particular amino acid at position 5 of SEQ. ID. NO. 9 is a cysteine residue. The recombinant Fc-OB sequence of SEQ. ID.

30 NO. 9 is a 378 amino acid Fc-OB protein (not counting the methionine residue). The first amino acid sequence for the recombinant Fc-OB protein of Figure 3 is referred to as +1 with the methionine at the -1 35 position.

One may remove the cysteine residue at position 5 or substitute it with one or more amino acids. An alanine residue may be substituted for the cysteine residue at position 6 giving the variant amino acid sequence of Figure 4 (SEQ. ID. NO. 12). The recombinant Fc-OB protein of Figure 4 is a 378 amino acid Fc-OB protein (not counting the methionine residue). The first amino acid sequence for the recombinant Fc-OB protein of Figure 4 is referred to as +1 with the methionine at the -1 position.

Likewise, the cysteine at position 5 of SEQ. ID. NO. 9 could be substituted with a serine or other amino acid residue or deleted. A variant or analog may also be prepared by deletion of amino acids at positions 1, 2, 3, 4 and 5 as with the variant in SEQ. ID. NO. 15 (See Figure 5). Substitutions at these positions can also be made and are within the scope of this invention. The recombinant Fc-OB protein of Figure 5 is a 373 amino acid Fc-OB protein (not counting the methionine residue). The first amino acid sequence for the recombinant Fc-OB protein of Figure 5 is referred to as +1 with the methionine at the -1 position.

Modifications may also be made to introduce four amino acid substitutions to ablate the Fc receptor binding site and the complement (C1q) binding site. These variant modifications from SEQ. ID. NO. 15 would include leucine at position 15 substituted with glutamate, glutamate at position 98 substituted with alanine, and lysines at positions 100 and 102 substituted with alanines (see Figure 6 and SEQ. ID. NO. 18). The recombinant Fc-OB protein of Figure 6 is a 373 amino acid Fc-OB protein (not counting the methionine residue). The first amino acid sequence for the recombinant Fc-OB protein of Figure 6 is referred to as +1 with the methionine at the -1 position.

Likewise, one or more tyrosine residues can be replaced by phenylalanine residues as well. In addition, other variant amino acid insertions, deletions and/or substitutions are also contemplated and are within the 5 scope of the present invention. Furthermore, alterations may be in the form of altered amino acids, such as peptidomimetics or D-amino acids. The Fc protein may be also linked to the OB proteins of the Fc-OB protein by "linker" moieties whether chemical or 10 amino acids of varying lengths. Such chemical linkers are well known in the art. Amino acid linker sequences can include but are not limited to:

- (a) ala, ala, ala;
- (b) ala, ala, ala, ala;
- 15 (c) ala, ala, ala, ala, ala;
- (d) gly, gly;
- (e) gly, gly, gly;
- (f) gly, gly, gly, gly, gly;
- (g) gly, gly, gly, gly, gly, gly, gly;
- 20 (h) gly-pro-gly;
- (i) gly, gly, pro, gly, gly; and
- (j) any combination of subparts (a)

through (i).

The OB portion of the Fc-OB fusion protein may 25 be selected from the recombinant murine set forth in SEQ. ID. NO. 3 (See Figure 1), or the recombinant human protein as set forth in Zhang et al., *Nature, supra*, (herein incorporated by reference) or those lacking a glutaminyl residue at position 28. (See Zhang et al., 30 *Nature, supra*, at page 428.) One may also use the recombinant human OB protein analog as set forth in SEQ. ID. NO. 6 (See Figure 2), which contains: (1) an arginine in place of lysine at position 35; and (2) a leucine in place of isoleucine at position 74. (A 35 shorthand abbreviation for this analog is the recombinant human R->L<sup>35</sup>, I->L<sup>74</sup>). The amino acid

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sequences for the recombinant human and recombinant murine proteins or analogs with or without the fused Fc portion at the N-terminus of the OB protein are set forth below with a methionyl residue at the -1 position; 5 however, as with any of the present OB proteins and analogs, the methionyl residue may be absent.

The murine protein is substantially homologous to the human protein, particularly as a mature protein, and, further, particularly at the N-terminus. One may 10 prepare an analog of the recombinant human protein by altering (such as substituting amino acid residues), in the recombinant human sequence, the amino acids which diverge from the murine sequence. Because the recombinant human protein has biological activity in 15 mice, such an analog would likely be active in humans. For example, using a human protein having a lysine at residue 35 and an isoleucine at residue 74 according to the numbering of SEQ. ID. NO. 6, wherein the first amino acid is valine, and the amino acid at position 146 is 20 cysteine, one may substitute with another amino acid one or more of the amino acids at positions 32, 35, 50, 64, 68, 71, 74, 77, 89, 97, 100, 105, 106, 107, 108, 111, 118, 136, 138, 142, and 145. One may select the amino acid at the corresponding position of the murine 25 protein, (SEQ. ID. NO. 3), or another amino acid.

One may further prepare "consensus" molecules based on the rat OB protein sequence. Murakami et al., Biochem. Biophys. Res. Comm. 209: 944-952 (1995) herein incorporated by reference. Rat OB protein differs from 30 human OB protein at the following positions (using the numbering of SEQ. ID. NO. 6): 4, 32, 33, 35, 50, 68, 71, 74, 77, 78, 89, 97, 100, 101, 102, 105, 106, 107, 108, 111, 118, 136, 138 and 145. One may substitute with another amino acid one or more of the amino acids at 35 these divergent positions. The positions in bold print are those in which the murine OB protein as well as the

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rat OB protein are divergent from the human OB protein, and thus, are particularly suitable for alteration. At one or more of a positions, one may substitute an amino acid from the corresponding rat OB protein, or another 5 amino acid.

The positions from both rat and murine OB protein which diverge from the mature human OB protein are: 4, 32, 33, 35, 50, 64, 68, 71, 74, 77, 78, 89, 97, 100, 102, 105, 106, 107, 108, 111, 118, 136, 138, 142, 10 and 145. An OB protein according to SEQ. ID. NO. 6 having one or more of the above amino acids replaced with another amino acid, such as the amino acid found in the corresponding rat or murine sequence, may also be effective.

15 In addition, the amino acids found in rhesus monkey OB protein which diverge from the mature human OB protein are (with identities noted in parentheses in one letter amino acid abbreviation): 8 (S), 35 (R), 48(V), 53(Q), 60(I), 66(I), 67(N), 68((L), 89(L), 100(L); 20 108(E), 112 (D), and 118 (L). Since the recombinant human OB protein is active in cynomolgus monkeys, a human OB protein according to SEQ. ID. NO. 6 (with lysine at position 35 and isoleucine at position 74) having one or more of the rhesus monkey divergent amino 25 acids replaced with another amino acid, such as the amino acids in parentheses, may be effective. It should be noted that certain rhesus divergent amino acids are also those found in the above murine species (positions 35, 68, 89, 100 and 112). Thus, one may prepare a 30 murine/rhesus/human consensus molecule having (using the numbering of SEQ. ID. NO. 6 having a lysine at position 35 and an isoleucine at position 74) having one or more of the amino acids at positions replaced by another amino acid: 4, 8, 32, 33, 35, 48, 50, 53, 60, 64, 66, 35 67, 68, 71, 74, 77, 78, 89, 97, 100, 102, 105, 106, 107, 108, 111, 112, 118, 136, 138, 142, and 145.

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Other analogs may be prepared by deleting a part of the protein amino acid sequence. For example, the mature protein lacks a leader sequence (-22 to -1). One may prepare the following truncated forms of human  
5 OB protein molecules (using the numbering of SEQ. ID. NO. 6):

- (a) amino acids 98-146
- (b) amino acids 1-32
- (c) amino acids 40-116
- 10 (d) amino acids 1-99 and (connected to)  
112-146
- (e) amino acids 1-99 and (connected to)  
112-146 having one or more of amino acids 100-111 placed between amino acids 99 and 112.

15 In addition, the truncated forms may also have altered one or more of the amino acids which are divergent (in the rat, murine, or rhesus OB protein) from human OB protein. Furthermore, any alterations may be in the form of altered amino acids, such as  
20 peptidomimetics or D-amino acids.

Therefore, the present invention encompasses a Fc-OB fusion protein wherein the OB protein is selected from:

- (a) the amino acid sequence 1-146 as set forth in SEQ. ID. NO. 3 (below) or SEQ. ID. NO. 6;
- (b) the amino acid sequence 1-146 as set forth in SEQ. ID. NO. 6 having a lysine residue at position 35 and an isoleucine residue at position 74;
- (c) the amino acid sequence of subpart (b)  
30 having a different amino acid substituted in one or more of the following positions (using the numbering according to SEQ. ID. NO. 6 and retaining the same numbering even in the absence of a glutamyl residue at position 28): 4, 32, 33, 35, 50, 64, 68, 71, 74, 77,  
35 78, 89, 97, 100, 102, 105, 106, 107, 108, 111, 118, 136, 138, 142, and 145;

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- (d) the amino acid sequence of subparts (a),  
(b) or (c) optionally lacking a glutaminyl residue at  
position 28;
- (e) the amino acid sequence of subparts (a),  
5 (b), (c), or (d) having a methionyl residue at the  
N-terminus;
- (f) a truncated OB protein analog selected  
from among: (using the numbering of SEQ. ID. NO. 6):
  - (i) amino acids 98-146
  - 10 (ii) amino acids 1-32
  - (iii) amino acids 40-116
  - (iv) amino acids 1-99 and 112-146
  - (v) amino acids 1-99 and 112-146 having  
one or more of amino acids 100-111 placed between  
15 amino acids 99 and 112; and,
  - (vi) the truncated OB analog of subpart  
(i) having one or more of amino acids 100, 102,  
105, 106, 107, 108, 111, 118, 136, 138, 142, and  
145 substituted with another amino acid;
  - 20 (vii) the truncated analog of subpart  
(ii) having one or more of amino acids 4, 8 and 32  
substituted with another amino acid;
  - (viii) the truncated analog of subpart  
25 (iii) having one or more of amino acids 50, 53, 60,  
64, 66, 67, 68, 71, 74, 77, 78, 89, 97, 100, 102,  
105, 106, 107, 108, 111 and 112 replaced with  
another amino acid;
  - (vix) the truncated analog of subpart  
30 (iv) having one or more of amino acids 4, 8, 32,  
33, 35, 48, 50, 53, 60, 64, 66, 67, 68, 71, 74, 77,  
78, 89, 97, 112, 118, 136, 138, 142, and 145  
replaced with another amino acid; and
  - (x) the truncated analog of subpart (v)  
having one or more of amino acids 4, 32, 33, 35,

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50, 64, 68, 71, 74, 77, 78, 89, 97, 100, 102, 105,  
106, 107, 108, 111, 118, 136, 138, 142, and 145  
replaced with another amino acid;

5 (xi) the truncated analog of any of  
subparts (i)-(x) having an N-terminal methionyl  
residue; and

10 (g) the OB protein or analog derivative of  
any of subparts (a) through (f) comprised of a chemical  
moiety connected to the protein moiety;

(h) a derivative of subpart (g) wherein said  
chemical moiety is a water soluble polymer moiety;

(i) a derivative of subpart (h) wherein said  
water soluble polymer moiety is polyethylene glycol;

15 (j) a derivative of subpart (h) wherein said  
water soluble polymer moiety is a polyaminoacid moiety;

(k) a derivative of subpart (h) through (j)  
wherein said moiety is attached at solely the N-terminus  
of said protein moiety; and

20 (l) an OB protein, analog or derivative of  
any of subparts (a) through (k) in a pharmaceutically  
acceptable carrier.

#### Derivatives

The present Fc-OB fusion proteins (herein the  
25 term "protein" is used to include "peptide," Fc, OB or  
analogs, such as those recited infra, unless otherwise  
indicated) are derivatized by the attachment of one or  
more chemical moieties to the Fc-OB fusion protein  
moiety. These chemically modified derivatives may be  
30 further formulated for intraarterial, intraperitoneal,  
intramuscular subcutaneous, intravenous, oral, nasal,  
pulmonary, topical or other routes of administration as  
discussed below. Chemical modification of biologically  
active proteins has been found to provide additional  
35 advantages under certain circumstances, such as  
increasing the stability and circulation time of the

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therapeutic protein and decreasing immunogenicity. See, U.S. Patent No. 4,179,337, Davis et al., issued December 18, 1979. For a review, see Abuchowski et al., in Enzymes as Drugs. (J. S. Holcerberg and J. Roberts, 5 eds. pp. 367-383 (1981)); Francis et al., supra.

The chemical moieties suitable for such derivatization may be selected from among various water soluble polymers. The polymer selected should be water soluble so that the protein to which it is attached does 10 not precipitate in an aqueous environment, such as a physiological environment. Preferably, for therapeutic use of the end-product preparation, the polymer will be pharmaceutically acceptable. One skilled in the art will be able to select the desired polymer based on such 15 considerations as whether the polymer/protein conjugate will be used therapeutically, and if so, the desired dosage, circulation time, resistance to proteolysis, and other considerations. For the present proteins and peptides, the effectiveness of the derivatization may be 20 ascertained by administering the derivative, in the desired form (i.e., by osmotic pump, or, more preferably, by injection or infusion, or, further formulated for oral, pulmonary or nasal delivery, for example), and observing biological effects as described 25 herein.

The water soluble polymer may be selected from the group consisting of, for example, polyethylene glycol, copolymers of ethylene glycol/propylene glycol, carboxymethylcellulose, dextran, polyvinyl alcohol, 30 polyvinyl pyrrolidone, poly-1, 3-dioxolane, poly-1,3,6-trioxane, ethylene/maleic anhydride copolymer, polyaminoacids (either homopolymers or random copolymers), and dextran or poly(n-vinyl pyrrolidone)polyethylene glycol, propylene glycol 35 homopolymers, polypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols and polyvinyl

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alcohol. Polyethylene glycol propionaldehyde may have advantages in manufacturing due to its stability in water. Also, succinate and styrene may also be used.

The OB or Fc proteins used to formulate the  
5 Fc-OB fusion protein, may be prepared by attaching polyaminoacids or branch point amino acids to the Fc or OB protein (or analogs) moiety. For example, the polyaminoacid may be an additional carrier protein which, like the Fc fused to the OB protein or OB analog  
10 of the present invention, serves to also increase the circulation half life of the protein in addition to the advantages achieved via the Fc-OB fusion protein above. For the present therapeutic or cosmetic purpose of the present invention, such polyaminoacids should be those  
15 which have or do not create neutralizing antigenic response, or other adverse responses. Such polyaminoacids may be selected from the group consisting of serum album (such as human serum albumin), an additional antibody or portion thereof (e.g. the Fc  
20 region), or other polyaminoacids, e.g. lysines. As indicated below, the location of attachment of the polyaminoacid may be at the N-terminus of the Fc-OB protein moiety, or C-terminus, or other places in between, and also may be connected by a chemical  
25 "linker" moiety to the Fc-OB protein.

The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between about 2 kDa and about 100 kDa (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight) for ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of  
30 sustained release desired, the effects, if any on biological activity, the ease in handling, the degree or  
35

lack of antigenicity and other known effects of the polyethylene glycol to a therapeutic protein or analog).

The number of polymer molecules so attached may vary, and one skilled in the art will be able to 5 ascertain the effect on function. One may mono-derivatize, or may provide for a di-, tri-, tetra- or some combination of derivatization, with the same or different chemical moieties (e.g., polymers, such as different weights of polyethylene glycols). The 10 proportion of polymer molecules to protein (or peptide) molecules will vary, as will their concentrations in the reaction mixture. In general, the optimum ratio (in terms of efficiency of reaction in that there is no excess unreacted protein or polymer) will be determined 15 by factors such as the desired degree of derivatization (e.g., mono, di-, tri-, etc.), the molecular weight of the polymer selected, whether the polymer is branched or unbranched, and the reaction conditions.

The chemical moieties should be attached to 20 the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those skilled in the art. E.g., EP 0 401 384 herein incorporated by reference (coupling PEG to G-CSF), see also Malik et al., Exp. 25 Hematol. 20: 1028-1035 (1992) (reporting pegylation of GM-CSF using tresyl chloride). For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as, a free amino or carboxyl group. Reactive groups are those 30 to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residue. Those having a free carboxyl group may include aspartic acid residues, glutamic acid 35 residues, and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group

for attaching the polyethylene glycol molecule(s). Preferred for therapeutic purposes is attachment at an amino group, such as attachment at the N-terminus or lysine group. Attachment at residues important for 5 receptor binding should be avoided if receptor binding is desired.

One may specifically desire N-terminally chemically modified Fc-OB fusion protein. Using polyethylene glycol as an illustration of the present 10 compositions, one may select from a variety of polyethylene glycol molecules (by molecular weight, branching, etc.), the proportion of polyethylene glycol molecules to protein (or peptide) molecules in the reaction mix, the type of pegylation reaction to be 15 performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally 20 pegylated material from a population of pegylated protein molecules. Selective N-terminal chemical modification may be accomplished by reductive alkylation which exploits differential reactivity of different types of primary amino groups (lysine versus the 25 N-terminal) available for derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl group containing polymer is achieved. For example, one may selectively 30 N-terminally pegylate the protein by performing the reaction at a pH which allows one to take advantage of the pK<sub>a</sub> differences between the ε-amino group of the lysine residues and that of the α-amino group of the N-terminal residue of the protein. By such selective 35 derivatization, attachment of a water soluble polymer to a protein is controlled: the conjugation with the

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polymer takes place predominantly at the N-terminus of the protein and no significant modification of other reactive groups, such as the lysine side chain amino groups, occurs. Using reductive alkylation, the water  
5 soluble polymer may be of the type described above, and should have a single reactive aldehyde for coupling to the protein. Polyethylene glycol propionaldehyde, containing a single reactive aldehyde, may be used.

An N-terminally monopegylated derivative is  
10 preferred for ease in production of a therapeutic. N-terminal pegylation ensures a homogenous product as characterization of the product is simplified relative to di-, tri- or other multi-pegylated products. The use of the above reductive alkylation process for  
15 preparation of an N-terminal product is preferred for ease in commercial manufacturing.

#### Complexes

The Fc-OB fusion protein, analog or derivative  
20 thereof may be administered complexed to a binding composition. Such binding composition may have the effect of prolonging the circulation time even further than that achieved with the Fc-OB fusion protein, analog or derivative. Such composition may be a protein  
25 (or synonymously, peptide). An example of a binding protein is OB protein receptor or portion thereof, such as a soluble portion thereof. Other binding proteins may be ascertained by examining OB protein or Fc-OB protein in serum, or by empirically screening for the  
30 presence of binding. Binding proteins used will typically not interfere with the ability of OB protein, Fc-OB fusion proteins, or analogs or derivatives thereof, to bind to endogenous OB protein receptor and/or effect signal transduction.

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Pharmaceutical Compositions

The present invention also provides methods of using pharmaceutical compositions of the Fc-OB fusion proteins and derivatives. Such pharmaceutical compositions may be for administration for injection, or for oral, pulmonary, nasal, transdermal or other forms of administration. In general, comprehended by the invention are pharmaceutical compositions comprising effective amounts of protein or derivative products of the invention together with pharmaceutically acceptable diluents, preservatives, solubilizers, emulsifiers, adjuvants and/or carriers. Such compositions include diluents of various buffer content (e.g., Tris-HCl, acetate, phosphate), pH and ionic strength; additives such as detergents and solubilizing agents (e.g., Tween 80, Polysorbate 80), anti-oxidants (e.g., ascorbic acid, sodium metabisulfite), preservatives (e.g., Thimersol, benzyl alcohol) and bulking substances (e.g., lactose, mannitol); incorporation of the material into particulate preparations of polymeric compounds such as polylactic acid, polyglycolic acid, etc. or into liposomes. Hylauronic acid may also be used, and this may have the effect of promoting sustained duration in the circulation. Such compositions may influence the physical state, stability, rate of *in vivo* release, and rate of *in vivo* clearance of the present proteins and derivatives. See, e.g., Remington's Pharmaceutical Sciences, 18th Ed. (1990, Mack Publishing Co., Easton, PA 18042) pages 1435-1712 which are herein incorporated by reference. The compositions may be prepared in liquid form, or may be in dried powder, such as lyophilized form. Implantable sustained release formulations are also contemplated, as are transdermal formulations.

Contemplated for use herein are oral solid dosage forms, which are described generally in Remington's Pharmaceutical Sciences, 18th Ed. 1990 (Mack

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Publishing Co. Easton PA 18042) at Chapter 89, which is herein incorporated by reference. Solid dosage forms include tablets, capsules, pills, troches or lozenges, cachets or pellets. Also, liposomal or proteinoid encapsulation may be used to formulate the present compositions (as, for example, proteinoid microspheres reported in U.S. Patent No. 4,925,673). Liposomal encapsulation may be used and the liposomes may be derivatized with various polymers (e.g., U.S. Patent No. 5,013,556). A description of possible solid dosage forms for the therapeutic is given by Marshall, K. In: *Modern Pharmaceutics* Edited by G. S. Banker and C. T. Rhodes Chapter 10, 1979, herein incorporated by reference. In general, the formulation will include the Fc-OB fusion protein (or analog or derivative), and inert ingredients which allow for protection against the stomach environment, and release of the biologically active material in the intestine.

Also specifically contemplated are oral dosage forms of the above derivatized proteins. Fc-OB fusion protein may be chemically modified so that oral delivery of the derivative is efficacious. Generally, the chemical modification contemplated is the attachment of at least one moiety to the protein (or peptide) molecule itself, where said moiety permits (a) inhibition of proteolysis; and (b) uptake into the blood stream from the stomach or intestine. Also desired is the increase in overall stability of the protein and increase in circulation time in the body. Examples of such moieties include: Polyethylene glycol, copolymers of ethylene glycol and propylene glycol, carboxymethyl cellulose, dextran, polyvinyl alcohol, polyvinyl pyrrolidone and polyproline. Abuchowski and Davis, Soluble Polymer-Enzyme Adducts. In: "Enzymes as Drugs", Hocenberg and Roberts, eds., Wiley-Interscience, New York, NY, (1981), pp. 367-383; Newmark, et al., J. Appl.

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Biochem. 4: 185-189 (1982). Other polymers that could be used are poly-1,3-dioxolane and poly-1,3,6-tioxocane. Preferred for pharmaceutical usage, as indicated above, are polyethylene glycol moieties.

5 For the Fc-OB fusion protein, analog or derivative, the location of release may be the stomach, the small intestine (e.g., the duodenum, jejunum, or ileum), or the large intestine. One skilled in the art has available formulations which will not dissolve in  
10 the stomach, yet will release the material in the duodenum or elsewhere in the intestine. Preferably, the release will avoid the deleterious effects of the stomach environment, either by protection of the Fc-OB fusion protein, analog or derivative, or by release of  
15 the biologically active material beyond the stomach environment, such as in the intestine.

To ensure full gastric resistance a coating impermeable to at least pH 5.0 is essential. Examples of the more common inert ingredients that are used as  
20 enteric coatings are cellulose acetate trimellitate (CAT), hydroxypropylmethylcellulose phthalate (HPMCP), HPMCP 50, HPMCP 55, polyvinyl acetate phthalate (PVAP), Eudragit L30D, Aquateric, cellulose acetate phthalate (CAP), Eudragit L, Eudragit S, and Shellac. These  
25 coatings may be used as mixed films.

A coating or mixture of coatings can also be used on tablets, which are not intended for protection against the stomach. This can include sugar coatings, or coatings which make the tablet easier to swallow.  
30 Capsules may consist of a hard shell (such as gelatin) for delivery of dry therapeutic i.e. powder; for liquid forms, a soft gelatin shell may be used. The shell material of cachets could be thick starch or other edible paper. For pills, lozenges, molded tablets or  
35 tablet triturates, moist massing techniques can be used.

The therapeutic can be included in the formulation as fine multiparticulates in the form of granules or pellets of particle size about 1 mm. The formulation of the material for capsule administration could also be as a powder, lightly compressed plugs or even as tablets. The therapeutic could be prepared by compression.

Colorants and flavoring agents may all be included. For example, the protein (or derivative) may be formulated (such as by liposome or microsphere encapsulation) and then further contained within an edible product, such as a refrigerated beverage containing colorants and flavoring agents.

One may dilute or increase the volume of the therapeutic with an inert material. These diluents could include carbohydrates, especially mannitol,  $\alpha$ -lactose, anhydrous lactose, cellulose, sucrose, modified dextrans and starch. Certain inorganic salts may be also be used as fillers including calcium triphosphate, magnesium carbonate and sodium chloride. Some commercially available diluents are Fast-Flo, Emdex, STA-Rx 1500, Emcompress and Avicell.

Disintegrants may be included in the formulation of the therapeutic into a solid dosage form. Materials used as disintegrates include but are not limited to starch including the commercial disintegrant based on starch, Explotab. Sodium starch glycolate, Amberlite, sodium carboxymethylcellulose, ultramylopectin, sodium alginate, gelatin, orange peel, acid carboxymethyl cellulose, natural sponge and bentonite may all be used. Another form of the disintegrants are the insoluble cationic exchange resins. Powdered gums may be used as disintegrants and as binders and these can include powdered gums such as agar, Karaya or tragacanth. Alginic acid and its sodium salt are also useful as disintegrants.

Binders may be used to hold the therapeutic agent together to form a hard tablet and include materials from natural products such as acacia, tragacanth, starch and gelatin. Others include methyl cellulose (MC), ethyl cellulose (EC) and carboxymethyl cellulose (CMC). Polyvinyl pyrrolidone (PVP) and hydroxypropylmethyl cellulose (HPMC) could both be used in alcoholic solutions to granulate the therapeutic.

An antifrictional agent may be included in the formulation of the therapeutic to prevent sticking during the formulation process. Lubricants may be used as a layer between the therapeutic and the die wall, and these can include but are not limited to; stearic acid including its magnesium and calcium salts, polytetrafluoroethylene (PTFE), liquid paraffin, vegetable oils and waxes. Soluble lubricants may also be used such as sodium lauryl sulfate, magnesium lauryl sulfate, polyethylene glycol of various molecular weights, Carbowax 4000 and 6000.

Glidants that might improve the flow properties of the drug during formulation and to aid rearrangement during compression might be added. The glidants may include starch, talc, pyrogenic silica and hydrated silicoaluminate.

To aid dissolution of the therapeutic into the aqueous environment a surfactant might be added as a wetting agent. Surfactants may include anionic detergents such as sodium lauryl sulfate, dioctyl sodium sulfosuccinate and dioctyl sodium sulfonate. Cationic detergents might be used and could include benzalkonium chloride or benzethonium chloride. The list of potential nonionic detergents that could be included in the formulation as surfactants are lauromacrogol 400, polyoxyl 40 stearate, polyoxyethylene hydrogenated castor oil 10, 50 and 60, glycerol monostearate, polysorbate 40, 60, 65 and 80, sucrose fatty acid ester,

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methyl cellulose and carboxymethyl cellulose. These surfactants could be present in the formulation of the protein or derivative either alone or as a mixture in different ratios.

5           Additives which potentially enhance uptake of the protein (or derivative) are for instance the fatty acids oleic acid, linoleic acid and linolenic acid.

10          Controlled release formulation may be desirable. The drug could be incorporated into an inert matrix which permits release by either diffusion or leaching mechanisms e.g., gums. Slowly degenerating matrices may also be incorporated into the formulation, e.g., alginates, polysaccharides. Another form of a controlled release of this therapeutic is by a method 15 based on the Oros therapeutic system (Alza Corp.), i.e., the drug is enclosed in a semipermeable membrane which allows water to enter and push drug out through a single small opening due to osmotic effects. Some enteric coatings also have a delayed release effect.

20          Other coatings may be used for the formulation. These include a variety of sugars which could be applied in a coating pan. The therapeutic agent could also be given in a film coated tablet and the materials used in this instance are divided into 2 25 groups. The first are the nonenteric materials and include methyl cellulose, ethyl cellulose, hydroxyethyl cellulose, methylhydroxy-ethyl cellulose, hydroxypropyl cellulose, hydroxypropyl-methyl cellulose, sodium carboxy-methyl cellulose, providone and the polyethylene glycols. The second group consists of the enteric 30 materials that are commonly esters of phthalic acid.

35          A mix of materials might be used to provide the optimum film coating. Film coating may be carried out in a pan coater or in a fluidized bed or by compression coating.

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Also contemplated herein is pulmonary delivery of the present protein (or derivatives thereof). The protein (or derivative) is delivered to the lungs of a mammal while inhaling and traverses across the lung epithelial lining to the blood stream. (Other reports of this include Adjei et al., Pharmaceutical Research 7: 565-569 (1990); Adjei et al., International Journal of Pharmaceutics 63: 135-144 (1990) (leuprolide acetate); Braquet et al., Journal of Cardiovascular Pharmacology 13 (suppl. 5): s.143-146 (1989) (endothelin-1); Hubbard et al., Annals of Internal Medicine 3: 206-212 (1989) ( $\alpha$ 1-antitrypsin); Smith et al., J. Clin. Invest. 84: 1145-1146 (1989) ( $\alpha$ -1-proteinase); Oswein et al., "Aerosolization of Proteins", Proceedings of Symposium on Respiratory Drug Delivery II, Keystone, Colorado, March, 1990 (recombinant human growth hormone); Debs et al., The Journal of Immunology 140: 3482-3488 (1988) (interferon- $\gamma$  and tumor necrosis factor  $\alpha$ ) and Platz et al., U.S. Patent No. 5,284,656 (granulocyte colony stimulating factor).

Contemplated for use in the practice of this invention are a wide range of mechanical devices designed for pulmonary delivery of therapeutic products, including but not limited to nebulizers, metered dose inhalers, and powder inhalers, all of which are familiar to those skilled in the art.

Some specific examples of commercially available devices suitable for the practice of this invention are the Ultravent nebulizer, manufactured by Mallinckrodt, Inc., St. Louis, Missouri; the Acorn II nebulizer, manufactured by Marquest Medical Products, Englewood, Colorado; the Ventolin metered dose inhaler, manufactured by Glaxo Inc., Research Triangle Park, North Carolina; and the Spinhaler powder inhaler, manufactured by Fisons Corp., Bedford, Massachusetts.

All such devices require the use of formulations suitable for the dispensing of protein (or analog or derivative). Typically, each formulation is specific to the type of device employed and may involve 5 the use of an appropriate propellant material, in addition to diluents, adjuvants and/or carriers useful in therapy.

The protein (or derivative) should most advantageously be prepared in particulate form with an 10 average particle size of less than 10  $\mu\text{m}$  (or microns), most preferably 0.5 to 5  $\mu\text{m}$ , for most effective delivery to the distal lung.

Carriers include carbohydrates such as trehalose, mannitol, xylitol, sucrose, lactose, and 15 sorbitol. Other ingredients for use in formulations may include DPPC, DOPE, DSPC and DOPC. Natural or synthetic surfactants may be used. Polyethylene glycol may be used (even apart from its use in derivatizing 20 the protein or analog). Dextrans, such as cyclodextran, may be used. Bile salts and other related enhancers may be used. Cellulose and cellulose derivatives may be used. Amino acids may be used, such as use in a buffer formulation.

Also, the use of liposomes, microcapsules or 25 microspheres, inclusion complexes, or other types of carriers is contemplated.

Formulations suitable for use with a nebulizer, either jet or ultrasonic, will typically comprise Fc-OB protein, analogs or derivatives thereof, 30 dissolved in water at a concentration of about 0.1 to 25 mg of biologically active protein per mL of solution. The formulation may also include a buffer and a simple sugar (e.g., for protein stabilization and regulation of osmotic pressure). The nebulizer formulation may also 35 contain a surfactant, to reduce or prevent surface

induced aggregation of the protein caused by atomization of the solution in forming the aerosol.

Formulations for use with a metered-dose inhaler device will generally comprise a finely divided powder containing the protein (or derivative) suspended in a propellant with the aid of a surfactant. The propellant may be any conventional material employed for this purpose, such as a chlorofluorocarbon, a hydrochlorofluorocarbon, a hydrofluorocarbon, or a hydrocarbon, including trichlorofluoromethane, dichlorodifluoromethane, dichlorotetrafluoroethanol, and 1,1,1,2-tetrafluoroethane, or combinations thereof. Suitable surfactants include sorbitan trioleate and soya lecithin. Oleic acid may also be useful as a surfactant.

Formulations for dispensing from a powder inhaler device will comprise a finely divided dry powder containing protein (or derivative) and may also include a bulking agent, such as lactose, sorbitol, sucrose, mannitol, trehalose, or xylitol in amounts which facilitate dispersal of the powder from the device, e.g., 50 to 90% by weight of the formulation.

Nasal delivery of the protein (or analog or derivative) is also contemplated. Nasal delivery allows the passage of the protein to the blood stream directly after administering the therapeutic product to the nose, without the necessity for deposition of the product in the lung. Formulations for nasal delivery include those with dextran or cyclodextran. Delivery via transport across other mucus membranes is also contemplated.

#### Dosage

One skilled in the art will be able to ascertain effective dosages by administration and observing the desired therapeutic effect. Due to the N-terminus modification of the OB protein, the present

invention provides unexpected protein protection from degradation, and increases circulation time and stability, when compared to OB protein or C-terminus modification of the OB protein. One skilled in the art, 5 therefore, will be able to ascertain from these changes that an effective dosage may require lower doses or less frequent dosing.

Preferably, the formulation of the molecule will be such that between about .10 µg/kg/day and 10 mg/kg/day will yield the desired therapeutic effect. The effective dosages may be determined using diagnostic tools over time. For example, a diagnostic for measuring the amount of OB protein or Fc-OB fusion protein in the blood (or plasma or serum) may first be 15 used to determine endogenous levels of protein. Such diagnostic tools may be in the form of an antibody assay, such as an antibody sandwich assay. The amount of endogenous OB protein is quantified initially, and a baseline is determined. The therapeutic dosages are 20 determined as the quantification of endogenous and exogenous OB protein or Fc-OB fusion protein (that is, protein, analog or derivative found within the body, either self-produced or administered) is continued over the course of therapy. The dosages may therefore vary 25 over the course of therapy, with a relatively high dosage being used initially, until therapeutic benefit is seen, and lower dosages used to maintain the therapeutic benefits.

Ideally, in situations where solely reduction 30 in blood lipid levels is desired, where maintenance of reduction of blood lipid levels is desired, or an increase in lean body mass is desired, the dosage will be insufficient to result in weight loss. Thus, during an initial course of therapy of an obese person, dosages 35 may be administered whereby weight loss and concomitant blood lipid level lowering or concomitant fat tissue

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decrease/lean mass increase is achieved. Once sufficient weight loss is achieved, a dosage sufficient to prevent re-gaining weight, yet sufficient to maintain desired blood lipid levels or lean mass increase (or, prevention of lean mass depletion) may be administered. These dosages can be determined empirically, as the effects of OB or Fc-OB protein are reversible, (e.g., Campfield et al., *Science* 269: 546-549 (1995) at 547). Thus, if a dosage resulting in weight loss is observed when weight loss is not desired, one would administer a lower dose in order to achieve the desired blood lipid levels or increase in lean tissue mass, yet maintain the desired weight.

For increasing an individual's sensitivity to insulin, similar dosage considerations may be taken into account. Lean mass increase without weight loss may be achieved sufficient to decrease the amount of insulin (or, potentially, amylin, thiazolidinediones, or other potential diabetes treating drugs) an individual would be administered for the treatment of diabetes.

For increasing overall strength, there may be similar dosage considerations. Lean mass increase with concomitant increase in overall strength may be achieved with doses insufficient to result in weight loss. Other benefits, such as an increase in red blood cells (and oxygenation in the blood) and a decrease in bone resorption or osteoporosis may also be achieved in the absence of weight loss.

### 30                  Combinations

The present methods may be used in conjunction with other medicaments, such as those useful for the treatment of diabetes (e.g., insulin, possibly, thiazolidinediones, amylin, or antagonists thereof), cholesterol and blood pressure lowering medicaments (such as those which reduce blood lipid levels or other

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cardiovascular medicaments), and activity increasing medicaments (e.g., amphetamines). Appetite suppressants may also be used (such as those affecting the levels of serotonin or neuropeptide Y). Such administration may be 5 simultaneous or may be in seriatim.

In addition, the present methods may be used in conjunction with surgical procedures, such as cosmetic surgeries designed to alter the overall appearance of a body (e.g., liposuction or laser 10 surgeries designed to reduce body mass). The health benefits of cardiac surgeries, such as bypass surgeries or other surgeries designed to relieve a deleterious condition caused by blockage of blood vessels by fatty deposits, such as arterial plaque, may be increased with 15 concomitant use of the present compositions and methods. Methods to eliminate gall stones, such as ultrasonic or laser methods, may also be used either prior to, during or after a course of the present therapeutic methods. Furthermore, the present methods may be used as an 20 adjunct to surgeries or therapies for broken bones, damaged muscle, or other therapies which would be improved by an increase in lean tissue mass.

The following examples are offered to more fully illustrate the invention, but are not to be 25 construed as limiting the scope thereof.

EXAMPLE 1: Use of Murine FC-OB Protein Via Subcutaneous Injection

This example demonstrates that injection 30 subcutaneously of murine Fc-OB protein results in weight loss in normal mice. Normal (non-obese) CD1 mice were administered murine Fc-OB protein via subcutaneous injections over a 22 day time period. A dosage of 10 mg protein/kg body weight/day resulted in a 14% (+/- 1.1%) 35 loss from baseline weight by the 22nd day of injections. A dosage of PBS resulted in a 3.9% (+/- 3.3%) loss from

baseline weight by the 22nd day of injections. The weight loss with the use of 10 mg protein/kg body weight/day of Fc-OB protein in obese CD1 mice resulted in a 10% (+/- 4.3%) loss from baseline weight and a 5 dosage of PBS resulted in a 8.7% (+/- 1.3%) loss from baseline weight, both by the 22nd day of injections

Presented below are the percent (%) differences from baseline weight in CD1 mice (8 weeks old):

10

Table 1

## Weight Loss Upon Subcutaneous Injection

Time (days)	Vehicle (PBS)	Lean/Recombinant Fc-OB Fusion Protein	Obese/Recombinant Fc-OB Fusion Protein
1-2	-.44 +/- 1.1	-3.6 +/- .41	-1.03 +/- 1.36
3-4	-1.07 +/- .13	-6.8 +/- 1.5	-2.7 +/- 1.1
5-6	-.13 +/- 1.1	-9.5 +/- 1.2	-4.9 +/- .95
7-8	-.92 +/- .29	-12.5 +/- 1.6	-7.7 +/- 2.9
9-10	1.6 +/- 1.3	-12.6 +/- 1.9	-8.2 +/- 2.9
11-12	-1.98 +/- 1	-13.6 +/- 1.96	-8.6 +/- 2.9
13-14	-5.2 +/- 1.3	-14.6 +/- 1.7	-10.1 +/- 3.6
15-16	-8.6 +/- 0.1	-14.5 +/- 2	-9.4 +/- 2.2
17-18	-8.5 +/- .64	-16.1 +/- 1.8	-9.6 +/- 2.99
19-20	-4.1 +/- .99	-16 +/- 1.5	-10.4 +/- 3.3
21-22	-3.9 +/- 3.3	-14.1 +/- 1.1	-10 +/- 4.3

15 As can be seen, at the end of a 22 day subcutaneous regime, animals receiving the FC-OB protein lost over 14.1% of their body weight in lean and 10% of body weight in obese, as compared to animals only receiving the PBS vehicle and as compared to baseline.

20 Surprisingly, animals receiving Fc-OB protein up to 22 days continued to loose weight up until 28

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days, 4 days after the last injection. Normal (non-obese) CD1 mice administered 10 mg protein/kg body weight/day of murine Fc-OB protein via subcutaneous injections stopped at day 22 resulted in a 21% loss from baseline weight at day 28 as compared to 14% loss at day 22. Likewise, obese CD1 mice administered 10 mg protein/kg body weight/day of murine Fc-OB protein stopped at day 22 resulted in a 13% loss from baseline weight at day 28 compared to 10% loss at day 22. At day 34 weight loss was maintained at 10% loss in obese mice where lean mice recovered to 5% loss. Controls in each system from day 22 through day 34 averaged from 4% in obese mice and 7% gain in lean mice.

15     EXAMPLE 2: Use of Human FC-OB Protein Via Subcutaneous Injection in C57 Mice

This example demonstrates that injection subcutaneously of human Fc-OB protein results in weight loss in normal mice. Normal (non-obese) C57 mice were administered human Fc-OB protein via subcutaneous injections over a 7 day time period. A dosage of 10 mg protein/kg body weight/day resulted in a 12% (+/- 1.3%) loss from baseline weight by the 7th day of injections. A dosage of 1 mg protein/kg body weight/day resulted in a 8.9% (+/- 1.5%) loss from baseline weight by the 7th day of injections. The weight loss with the use of 10 mg protein/kg body weight/day of human OB protein in obese C57 mice resulted in a 1.1% (+/- .99%) loss from baseline weight and a dosage of 1 mg protein/kg body weight/day resulted in a 2.5% (+/- 1.1%) loss from baseline weight, both by the 7th day of injections.

Results

Presented below are the percent (%) differences from baseline weight in C57 mice (8 weeks old):

Table 2  
Weight Loss Upon Subcutaneous Injection

Time (days)	Vehicle (PBS)	Recombinant Fc-OB Fusion Protein	Recombinant OB Protein
1-2	.258 +/- 1.3	-6.4 +/- 1.6	-2.1 +/- .91
3-4	2.2 +/- 1.1	-12.1 +/- 1.5	-.78 +/- .36
5-6	4.5 +/- 2	-11.5 +/- 1.5	-1.7 +/- .6
7-8	7.0 +/- 2.1	-11.9 +/- 1.6	0.1 +/- 1.2
9-10	9.0 +/- 1.9	-11.5 +/- 1.3	7.2 +/- 2.7
11-12	10 +/- 3.8	-9 +/- 1.4	10.9 +/- 2.9
13-14	12.5 +/- 4.4	-9.5 +/- 1.6	12.3 +/- 6.4
15-16	11.1 +/- 1.0	-3.0 +/- 1.5	10.3 +/- 3.3
17-18	17.2 +/- 3.6	8.0 +/- 1.3	13.3 +/- 3.4

5           As can be seen, at the end of a day 17 after a  
 7 day subcutaneous regime at 10 mg/kg/day, animals  
 receiving the FC-OB protein recovered to 8% of their  
 body weight. Animals receiving dosages of 1 mg/kg/day  
 after a 7 day subcutaneous regime returned to 6.4% of  
 10 body weight after 12 days.

15           These studies also show that during recovery  
 periods from day 7 to day 22, after the last injection  
 at day 7, body weight recovery is slower in the Fc-OB  
 treated C57 mice than with the OB treated mice. This  
 suggests that the Fc-OB protein is not cleared as  
 quickly as OB protein thereby causing the extended  
 weight loss effect.

EXAMPLE 3: Dose Response of CF7 Mice Treated with Fc-OB  
20          Fusion Protein

An additional study demonstrated that there  
 was a dose response to continuous administration of  
 Fc-OB protein. In this study, obese CF7 mice, weighing

35-40 g were administered recombinant human Fc-OB protein using methods similar to the above example. The results are set forth in Table 3, below, (with % body weight lost as compared to baseline, measured as above):

5

Table 3  
Dose Response With Continuous Administration

Dose	Time	% Reduction in Body Weight
0.25 mg/kg/day	Day 5	4
0.5 mg/kg/day	Day 5	12
1 mg/kg/day	Day 5	16

10 As can be seen, increasing the dose from 0.25 mg/kg/day to 1 mg/kg/day increased the weight lost from 4% to 16%. It is also noteworthy that at day 5, the 1 mg/kg/day dosage resulted in a 16% reduction in body weight. These studies also showed slow weight recovery 15 rates to 0% suggesting that the Fc-OB protein is not quickly cleared thereby causing the extended weight loss effect.

EXAMPLE 4: Pharmacokinetics of recombinant human Fc-OB  
20 in CD-1 Mice and Dogs

This study demonstrated the pharmacokinetic properties of recombinant human met Fc-OB protein in CD-1 mice and dogs. Following intravenous or subcutaneous dosing at 1 mg/kg/day, serum concentrations 25 of recombinant human met Fc-OB protein and human met OB protein were determined by an enzyme-linked immunosorbent assay (ELISA).

In both species, an increase in exposure, as quantified by higher peak serum concentrations and 30 larger areas under-the-serum-concentration-curve (AUC), was observed when compared to recombinant met-human OB

protein. Fc-OB has lower systemic clearance than recombinant met-human OB protein. This is seen in the lower clearance and longer half-life of Fc-OB over OB protein. The increase in size causes not only an 5 increase in protein stability, but also a decrease in the efficiency of renal clearance. As a result, Fc-OB is cleared slower from the systemic circulation. The increases in peak time, peak serum concentrations and AUC for Fc-OB protein are consistent with lower 10 clearance. Fc-OB protein will yield substantially higher systemic exposure when compared to OB protein. Results are shown in Table 4 below:

Table 4

## 15 Pharmacokinetic Properties

Species	CD-1 Mice		CD-1 Mice		Beagle Dogs	
Route of Administration	Intravenous		Subcutaneous		Subcutaneous	
	OB protein	Fc-OB protein	OB protein	Fc-OB protein	OB protein	Fc-OB protein
Dose Level (mg/kg)	1	1	1	1	0.5	0.5
Peak Time (h)			0.14	6	2.8	8
Peak Serum Concentration (ng/mL)			1520	7550	300	1120
AUC (ng·h/mL)	1470	366000	1230	132000	2200	52500
Half-life (h)	0.491	21.4	0.388		2.13	22.9
Clearance (mL/h/kg)	681	2.73				

EXAMPLE 5:

This example demonstrates that in normal mice 20 which are not obese and do not have elevated blood lipid levels, administration of human recombinant Fc-OB

protein results in a lowering of cholesterol, glucose and triglyceride levels. In addition, this example demonstrates that these levels remain low over a three day recovery period.

5           Normal CD1 mice were administered recombinant human Fc-OB protein via subcutaneous injections. Blood samples were taken 24 hours after day 23, the last day of injection. As discussed above, the animals lost weight at the dosages administered. As shown in Table  
 10 5, the mice had substantial reduction of serum cholesterol, glucose and triglycerides in a dose-dependent fashion when compared to controls:

Table 5

15

Dose	Glucose	Cholesterol	Triglycerides
PBS	232.6 +/- 15.1	67.8 +/- 3.6	52.6 +/- 3.7
1 mg/kg/day	225.8 +/- 29.1	54 +/- 5.6	43 +/- 8.7
10 mg/kg/day	193.2 +/- 21.4	53.4 +/- 5.7	38 +/- 11
1 mg/kg every 2 days	242.0 +/- 9.3	52.6 +/- 4.4	40.8 +/- 7.2
10 mg/kg every 2 days	197.4 +/- 27.9	51.4 +/- 5.9	29.8 +/- 6.3
1 mg/kg every 3 days	244.8 +/- 19.5	60.8 +/- 7.3	54 +/- 7.1
10 mg/kg every 3 days	188 +/- 31.2	52.2 +/- 6.9	26.2 +/- 10.7

These data demonstrate that the Fc-OB protein, or analogs or derivatives thereof, are effective blood lipid lowering agents.

20

EXAMPLE 6:

A obese human patient is administered human Fc-OB protein, or analog or derivative for the purpose of weight reduction. The obese patient also has elevated

levels of blood lipids, including elevated levels of cholesterol, above 200 mg/100 ml. The patient attains a satisfactory weight reduction over the course of Fc-OB therapy. A maintenance dose of Fc-OB protein or analog or derivative is administered to the non-obese patient to maintain lowered blood lipid levels, including lowered cholesterol levels, below 200 mg/100 ml. The dose administered is insufficient to result in further weight loss. Administration is chronic. Levels of circulating Fc-OB protein or analog or derivative may be monitored using a diagnostic kit, such as an antibody assay against the OB protein (or other antigenic source if applicable).

15 EXAMPLE 7:

A non-obese human patient undergoes coronary bypass surgery or other invasive treatment to alleviate advanced stages arterial plaque formation. After the surgery, the patient is administered a maintenance dose of Fc-OB protein or analog or derivative in order to prevent the re-formation of arterial plaque. The dose administered is insufficient to result in weight loss. Administration is chronic. Levels of circulating Fc-OB protein or analog or derivative may be monitored using a diagnostic kit, such as an antibody assay against the OB protein (or other antigenic source if applicable).

EXAMPLE 8:

30 A non-obese human patient experiences hypertension due to restricted blood flow from clogged arteries. The patient is administered a dose of Fc-OB protein, or analog or derivative thereof sufficient to reduce arterial plaque resulting in clogged arteries. Thereafter, the patient is monitored for further 35 arterial plaque formation, and hypertension. If the condition reappears, the patient is re-administered an

effective amount of Fc-OB protein, analog or derivative sufficient to restore blood flow, yet insufficient to result in weight loss. Levels of circulating Fc-OB protein or analog or derivative may be monitored using a  
5 diagnostic kit, such as an antibody assay against the Fc-OB protein (or other antigenic source if applicable).

EXAMPLE 9:

A human patient experiences gall stones.  
10 Either the gall stones are not removed and the formation of additional gall stones is sought to be avoided, or the gall stones are removed but the gall bladder remains (as, for example, using laser or ultrasonic surgery) and the formation of additional gall stones is sought to be  
15 avoided. The patient is administered an effective amount of Fc-OB protein, analog or derivative thereof to result in prevention of accumulation of additional gall stones or re-accumulation of gall stones. Levels of circulating Fc-OB protein or analog or derivative may be  
20 monitored using a diagnostic kit, such as an antibody assay against the Fc-OB protein (or other antigenic source if applicable).

EXAMPLE 10:

25 A diabetic human patient desires to use decreased dosages of insulin for treatment of diabetes. The patient is administered an effective amount of Fc-OB protein, analog or derivative thereof to result in an increase in lean tissue mass. The patient's sensitivity  
30 to insulin increases, and the dosage of insulin necessary to alleviate symptoms of diabetes is decreased, either in terms of a decrease in the units of insulin needed, or in terms of a decrease in the number of injections of insulin needed per day. Levels of  
35 circulating Fc-OB protein or analog or derivative may be

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monitored using a diagnostic kit, such as an antibody assay against the OB protein (or other antigenic source if applicable).

5    EXAMPLE 11:

A non-obese human patient desires an increase in lean tissue mass for therapeutic purposes, such as recovery from illness which depleted lean tissue mass. The patient is administered an effective amount of Fc-OB 10 protein, analog or derivative thereof to result in the desired increase in lean tissue mass. Increase in lean tissue mass is monitored using DEXA scanning. Levels of circulating Fc-OB protein or analog or derivative may be monitored using a diagnostic kit, such as an antibody 15 assay against the OB protein (or other antigenic source if applicable).

MATERIALS AND METHODS

20            Animals. Wild type CD1 mice and (+/+) C57B16 mice were used for the above examples. The age of the mice at the initial time point was 8 weeks, and the animals were weight stabilized.

25            Feeding and Weight Measurement. Mice were given ground rodent chow (PMI Feeds, Inc.) in powdered food feeders (Allentown Caging and Equipment) which allowed a more accurate and sensitive measurement than use of regular block chow. Weight was measured at the 30 same time each day (2:00 p.m.), for the desired period. Body weight on the day prior to the injection was defined as baseline weight. The mice used weighed 18-22 grams.

35            Housing. Mice were single-housed, and maintained under humane conditions.

5        Administration of Protein or Vehicle. Protein  
          (as described below) or vehicle (phosphate buffered  
          saline, pH 7.4) were administered by subcutaneous  
          injections or intravenously.

10      Controls. Control animals were those who were  
          injected with the vehicle alone without either Fc-OB  
          fusion protein or OB protein added to the vehicle.

15      Protein. Sequence ID. Nos. 1, 2 and 3 set  
          forth murine recombinant OB DNA and protein (Figure 1),  
          and Sequence ID. Nos. 4, 5 and 6 set forth an analog  
          recombinant human OB DNA and protein (Figure 2). As noted  
          above recombinant human OB protein as in SEQ. ID.. NO. 6  
          has a lysine residue at position 35 and an isoleucine  
          residue at position 74. Furthermore, the recombinant  
          human protein set forth in Zhang et al., *Nature, supra*,  
          and PCT publication WO 96/05309 (12/22/96) (both  
          20     incorporated by reference including figures), and the  
          murine and human analog recombinant proteins of Figures 1  
          and 2 are illustrative of the OB protein which may be used  
          in forming the Fc-OB fusion protein of the present methods  
          of treatment and manufacture of a medicament. Other OB or  
          25     Fc proteins or analogs or derivatives thereof may also be  
          used to form the Fc-OB fusion protein.

30      Herein, the first amino acid of the amino acid  
          sequence for recombinant OB protein is referred to as  
          +1, and is valine, and the amino acid at position -1 is  
          methionine. The C-terminal amino acid is number 146  
          (cysteine) (see Figures 1 and 2). The first amino acid  
          sequence for recombinant human Fc-OB protein of Figure 3  
          is referred to as +1, and is glutamate, and the amino  
          acid at position -1 is methionine. The C-terminal amino  
          35     acid is number 378 (cysteine). The first amino acid  
          sequence for the recombinant human Fc-OB prot in variant

of Figure 4 is referred to as +1, and is glutamate, and the amino acid at position -1 is methionine. The C-terminal amino acid is number 378 (cysteine). The first amino acid sequence for the recombinant human  
5 Fc-OB protein variant of Figure 5 is referred to as +1, and is aspartic acid, and the amino acid at position -1 is methionine. The C-terminal amino acid is number 373 (cysteine). The first amino acid sequence for the recombinant human Fc-OB protein variant of Figure 6 is  
10 referred to as +1, and is aspartic acid, and the amino acid at position -1 is methionine. The C-terminal amino acid is number 373 (cysteine).

Expression Vector and Host Strain

15 The plasmid expression vector used is pAMG21 (ATCC accession number 98113), which is a derivative of pCFM1656 (ATCC accession number 69576) and contains appropriate restriction sites for insertion of genes downstream from the lux PR promoter (see US Patent No.  
20 5,169,318 for a description of the lux expression system). The Fc-OB DNA, described below and shown in Figures 3-6, was created and ligated into the expression vector pAMG21 linearized with restriction endonucleases NdeI and BamHI and transformed into the *E. coli* host  
25 strain, FM5. *E. coli* FM5 cells were derived at Amgen Inc., Thousand Oaks, CA from *E. coli* K-12 strain (Bachmann, et al., Bacterial. Rev. 40: 116-167 (1976)) and contain the integrated lambda phage repressor gene, cI857 (Sussman et al., C. R. Acad. Sci. 254: 1517-1579  
30 (1962)). Vector production, cell transformation, and colony selection were performed by standard methods, (e.g., Sambrook, et al., Molecular Cloning: A Laboratory Manual, 2d Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.) Host cells  
35 were grown in LB media.

Fc-OB DNA Construction

The plasmid pFc-A3 (described below) served as the source of sequence for human immunoglobulin IgG-1 heavy chain from amino acid number 99 (Glu) to the 5 natural carboxyl terminus. The human IgG-1 sequence can be obtained from Genebank (P01857).

The human OB sequence is disclosed above as well as Zhang et al., Nature, supra, and PCT publication WO 96/05309 both incorporated by reference including 10 drawings. The OB DNA was ligated into the expression vector pCFM1656 linearized with restriction endonucleases XbaI and BamHI using standard cloning procedures, e.g., Sambrook, et al., Molecular Cloning: A Laboratory Manual, 2d Edition, Cold Spring Harbor 15 Laboratory Press, Cold Spring Harbor, N.Y.. The plasmid pCFM1656 carrying the OB DNA sequence served as the source of sequence for the recombinant human OB gene.

The genetic fusing of these two sequences was carried out by the method of PCR overlap extension (Ho, 20 S.N., et al., Site Directed Mutagenesis By Overlap Extension Using The Polymerase Chain Reaction, Gene 77:51-59 (1989)). The product of the PCR was cleaved with restriction endonuclease NdeI to create a 5'-cohesive end and with restriction endonuclease BamHI 25 to create a 3'-cohesive terminus. The vector, pAMG21, was similarly cleaved. A ligation was performed with the fusion fragment and the linearized vector. Ligated DNA was transformed by electroporation into the *E. coli* host strain. Clones surviving on kanamycin (50 $\mu$ g/ml) 30 selection agar plates were checked for expression of Fc-OB-sized protein. Plasmid from individual clones was isolated and the sequence of the gene coding region verified.

When additional modifications of the Fc-OB 35 gene were desired, the PCR technique was used again to engineer the changes. Two sets of changes were

performed at the N-terminus of the Fc portion of the fusion protein (SEQ. ID. No. 9) to create the variants SEQ. ID. NOS. 12 and 15. Another variant was constructed to introduce four amino acid substitutions  
5 to ablate the Fc-receptor binding site (leucine at position 15 substituted with glutamate), and the complement (C1q) binding site (glutamate at position 98 substituted with alanine, lysine at position 100 substituted with alanine, and lysine at position 102 substituted with alanine (See, Xin Xiao Zheng et. al, J. Immunol. 154: 5590-5600 (1995)). The template for  
10 this construct was Seq. ID. No. 15 and the resulting variant was SEQ. ID. Nos. 18.

15                   pFc-A3 Vector Construction

A plasmid, pFc-A3, containing the region encoding the Fc portion of human immunoglobulin IgG-1 heavy chain (See Ellison, J. W. et. al, Nucleic Acids Res. 10:4071-4079 (1982)), from the first amino acid 20 Glu-99 of the hinge domain to the carboxyl terminus plus a 5'-NotI fusion site and 3'-SalI and XbaI sites, was made by PCR amplification of the human spleen cDNA library. PCR reactions were in a final volume of 100 ml and employed 2 units of Vent DNA polymerase in 20 mM Tris-HCl (pH 8.8), 10 mM KCl, 10 mM (NH4)2SO4, 2 mM MgSO4, 0.1% Triton X-100 with 400 mM each dNTP and 1 ng 25 of the cDNA library to be amplified together with 1 uM of each primer. Reactions were initiated by denaturation at 95 °C for 2 min, followed by 30 cycles of 95 °C for 30 s, 55 °C for 30 s, and 73 °C for 2 min. The 5'-primer incorporated a NotI site immediately 5' to the first residue (Glu-99) of the hinge domain of IgG-1. The 3'-primer incorporated SalI and XbaI sites. The 717 base pair PCR product was digested with NotI and SalI, 30 the resulting DNA fragment was isolated by electrophoresis through 1% agarose and purified and

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cloned into NotI, SalI-digested pBluescript II KS vector (Stratagene). The insert in the resulting plasmid, pFc-A3, was sequenced to confirm the fidelity of the PCR reaction.

5

Methods for Production

The methods below for production have been used to produce biologically active recombinant methionyl murine or human analog OB protein and Fc-OB fusion proteins. Similar 10 methods may be used to prepare biologically active methionyl human OB protein.

Fermentation Process

A batch fermentation process was used. Media 15 compositions are set forth below.

A portion of the media consisting of primarily nitrogen sources was sterilized (by raising temperature to 120~123°C for 25~35 minutes) in the fermentation vessel. Upon cooling, carbon, magnesium, phosphate, and 20 trace metal sources were added aseptically. An overnight culture of the above recombinant murine protein-producing bacteria of 500 mL (grown in LB broth) was added to the fermentor. When the culture optical density (measured at 600 nm as an indicator for cell 25 density) reached 15~25 absorption units, an autoinducer solution (0.5 mg/mL homoserine lactone) was added (1 mL/L) to the culture to induce the recombinant gene expression. The fermentation process was allowed to continue for additional 10 to 16 hours, followed by 30 harvesting the broth by centrifugation.

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Media Composition:

Batch:	34 g/L	Yeast extract
	78 g/L	Soy peptone
	0.9 g/L	Potassium chloride
5	5.0 g/L	Hexaphos
	1.7 g/L	Citric acid
	120 g/L	Glycerol
	0.5 g/L	MgSO <sub>4</sub> · 7H <sub>2</sub> O
	0.2 mL/L	Trace Metal Solution
10	0.5 mL/L	P2000 Antifoam

Trace Metal Solution:

	Ferric Chloride (FeCl <sub>3</sub> · 6H <sub>2</sub> O):	27 g/L
	Zinc Chloride (ZnCl <sub>2</sub> · 4H <sub>2</sub> O):	2 g/L
15	Cobalt Chloride (CoCl <sub>2</sub> · 6H <sub>2</sub> O):	2 g/L
	Sodium Molybdate (NaMoO <sub>4</sub> · 2H <sub>2</sub> O):	2 g/L
	Calcium Chloride (CaCl <sub>2</sub> · 2H <sub>2</sub> O):	1 g/L
	Cupric Sulfate (CuSO <sub>4</sub> · 5H <sub>2</sub> O):	1.9 g/L
	Boric Acid (H <sub>3</sub> BO <sub>3</sub> ):	0.5 g/L
20	Manganese Chloride (MnCl <sub>2</sub> · 4H <sub>2</sub> O):	1.6 g/L
	Sodium Citrate dihydrate:	73.5 g/L

Purification Process for Human Fc-OB Fusion

Protein

Purification for human Fc-OB fusion protein was accomplished by the steps below (unless otherwise noted, the following steps were performed at 4°C). Purification for murine and human OB protein is disclosed in PCT publication WO 96/05309, supra, herein incorporated by reference.

1. Cell paste. E. coli cell paste was suspended in 5 times volumes of distilled water. The cells in the water were further broken by two passes

through a microfluidizer. The broken cells were centrifuged at 4.2k rpm for 1 hour in a Beckman JB-6 centrifuge with a J5-4.2 rotor.

2. Inclusion body wash. The supernatant from 5 above was removed and the pellet was resuspended with five volumes of distilled water. The mixture was centrifuged as in step 1.

3. Solubilization. The pellet was solubilized with 10 volumes of 50 mM tris, pH 8.5, 8 M guanidine 10 hydrochloride, 10 mM dithiothreitol and stirred for one hour at room temperature. The solution is made 40 mM cystamine dihydrochloride and stirred for one hour.

4. The solution from step 3 is added to 20 to 30 volumes of the following refold solution: 50 mM tris, 15 pH 8.5, 0.8 M arginine, 2 M urea, and 4 mM cysteine. The refold is stirred for 16 hours at 8°C.

5. Buffer exchange. The solution from step 4 is concentrated and diafiltered into 10 mM tris, pH 8.5.

6. Acid precipitation. The solution from step 20 5 is adjusted to pH 4.75 with 50% glacial acid and incubated for 30 minutes at room temperature. The solution is filtered.

7. Cation exchange chromatography. The solution from step 6 is adjusted to pH 7.0 and loaded 25 onto a CM Sepharose Fast Flow column at 10°C. A twenty column volume gradient is done at 10 mM phosphate, pH 7.0, 0 to 0.1 M NaCl.

8. Anion exchange chromatography. The CM elution pool from step 7 is diluted 5 fold with 5 mM 30 tris, pH 7.5 and loaded onto a Q Sepharose Fast Flow at 10°C. A 20 column volume gradient is done at 10 mM tris, pH 7.5, 0 to 0.2M NaCl.

9. Hydrophobic interaction chromatography. The Q sepharose pool is made 0.75M ammonium sulfate and 35 loaded on a methyl Macroprep hydrophobic interaction

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column at room temperature. A 20 column volume gradient is done at 10 mM phosphate, pH 7.0, 0.75M to 0M ammonium sulfate.

10. Buffer exchange. The pool from step 9 is  
5 concentrated as necessary and dialyzed against PBS buffer.

While the present invention has been described in terms of preferred embodiments, it is understood that 10 variations and modifications will occur to those skilled in the art. Therefore, it is intended that the appended claims cover all such equivalent variations which come within the scope of the invention as claimed.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Mann, Michael B.  
Hecht, Randy I.
- (ii) TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND METHODS
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Amgen Inc.
  - (B) STREET: 1840 DeHavilland Drive
  - (C) CITY: Thousand Oaks
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 91320-1789
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/770,973
  - (B) FILING DATE: 20-DEC-1996
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Knight, Matthew W.
  - (B) REGISTRATION NUMBER: 36,846
  - (C) REFERENCE/DOCKET NUMBER: A-416

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 491 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 41
  - (D) OTHER INFORMATION: /n te= "Met = ATG"

- 50 -

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTAGATTTG AGTTTTAACT TTTAGAAGGA GGAATAACAT ATGGTACCGA TCCAGAAAGT	60
TCAGGACGAC ACCAAAACCT TAATTAAAAC GATCGTTACG CGTATCAACG ACATCAGTCA	120
CACCCAGTCG GTCTCCGCTA AACAGCGTGT TACCGGTCTG GACTTCATCC CGGGTCTGCA	180
CCCGATCCTA AGCTTGTCCA AAATGGACCA GACCCTGGCT GTATACCAGC AGGTGTTAAC	240
CTCCCCTGCCG TCCCAGAACG TTCTTCAGAT CGCTAACGAC CTCGAGAACCC TTCCGGACCT	300
GCTGCACCTG CTGGCATTCT CCAAATCCTG CTCCCCTGCCG CAGACCTCAG GTCTTCAGAA	360
ACCGGAATCC CTGGACGGGG TCCTGGAAGC ATCCCTGTAC AGCACCGAAG TTGTTGCTCT	420
GTCCCCGTCTG CAGGGTTCCC TTCAGGACAT CCTTCAGCAG CTGGACGTTT CTCCGGAATG	480
TTAATGGATC C	491

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGATCTAAAC TCAAAATTGA AAACTTCCT CCTTATTGTA TACCATGGCT AGGTCTTTCA	60
AGTCCTGCTG TGGTTTGGA ATTAAATTG CTAGCAATGC GCATAGTTGC TGTAGTCAGT	120
GTGGGTCAAGC CAGAGGCGAT TTGTCGCACA ATGCCAGAC CTGAAGTAGG GCCCAGACGT	180
GGGCTAGGAT TCGAACAGGT TTIACTGGT CTGGGACCGA CATATGGTCG TCCACAATTG	240
GAGGGACGGC AGGGTCTTGC AAGAAGTCTA GCGATTGCTG GAGCTCTTGG AAGCGCTGGA	300
CGACGTGGAC GACCGTAAGA GGTTTAGGAC GAGGGACGGC GTCTGGAGTC CAGAAGTCTT	360
TGGCCTTAGG GACCTGCCCG AGGACCTTCG TAGGGACATG TCGTGGCTTC AACAAACGAGA	420
CAGGGCAGAC GTCCCAAGGG AAGTCCTGTA GGAAGTCGTC GACCTGAAA GAGGCCTTAC	480
AATTACCTAG G	491

- 51 -

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met (ATG) starts at -1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys  
1 5 10 15

Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser  
20 25 30

Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro  
35 40 45

Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln  
50 55 60

Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp  
65 70 75 80

Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser  
85 90 95

Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp  
100 105 110

Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser  
115 120 125

Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser  
130 135 140

Pro Glu Cys  
145

- 52 -

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Met = ATG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CATATGGTAC CGATCCAGAA AGTCAGGAC GACACCAAAA CCTTAATTAA AACGATCGTT	60
ACCGGTATCA ACGACATCAG TCACACCCAG TCGGTGAGCT CTAAACAGCG TGTTACAGGC	120
CTGGACTTCA TCCCCGGTCT GCACCCGATC CTGACCTTGT CCAAAATGGA CCAGACCCCTG	180
GCTGTATAACC AGCAGATCTT AACCTCCATG CCGTCCCCGTA ACGTTCTTCA GATCTCTAAC	240
GACCTCGAGA ACCTTCGCGA CCTGCTGCAC GTGCTGGCAT TCTCCAATC CTGCCACCTG	300
CCATGGGCTT CAGGTCTTGA GACTCTGGAC TCTCTGGGGG GGGTCCTGGA AGCATCCGGT	360
TACAGCACCG AAGTTGTTGC TCTGTCCCGT CTGCAGGGTT CCCTTCAGGA CATGCTTTCGG	420
CAGCTGGACC TGTCTCCGGG TTGTTAATGG ATCC	454

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTATACCATG CCTAGGTCTT TCAAGTCTG CTGTGGTTTT GGAATTAATT TTGCTAGCAA	60
TGCGCATAGT TGCTGTAGTC AGTGTGGTC AGCCACTCGA GATTTGTGCG ACAATGTCCG	120

- 53 -

GACCTGAAGT AGGGCCCAGA CGTGGGCTAG GACTGGAACA GGTTTTACCT GGTCTGGGAC	180
CGACATATGG TCGTCTAGAA TTGGAGGTAC GGCAGGGCAT TGCAAGAAGT CTAGAGATTG	240
CTGGAGCTCT TGGAAGCGCT GGACGACGTG CACGACCGTA AGAGGTTAG GACGGTGGAC	300
GGTACCCGAA GTCCAGAACT CTGAGACCTG AGAGACCCGC CCCAGGACCT TCGTAGGCCA	360
ATGTCGTGGC TTCAACAAACG AGACAGGGCA GACGTCCCAA GGGAAAGTCCT GTACGAAACC	420
GTCGACCTGG ACAGAGGGCCC AACAAATTACC TAGG	454

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met (ATG) starts at -1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys			
1	5	10	15
Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser			
20	25	30	
Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro			
35	40	45	
Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln			
50	55	60	
Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn Asp			
65	70	75	80
Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser			
85	90	95	
Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly			
100	105	110	

- 54 -

Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser  
 115                    120                    125

Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser  
 130                    135                    140

Pro Gly Cys  
 145

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Met = ATG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CATATGGAAC CCAAATCTTG TGACAAAACT CACACATGCC CACCGTGC	60
CC CTCCTGGGGG GACCGTCAGT CTTCTCTTC CCCCCAAAAC CCAAGGACAC CCTCATGATC	120
TCCC GGACCC CTGAGGTAC AC ATGCGTGGTG GTGGACGTGA GCCACGAAGA CCCTGAGGTC	180
AAGTTCAACT GGTACGTGGA CGGGCGTGGAG GTGCATAATG CCAAGACAAA GCGCGGGAG	240
GAGCAGTACA ACAGCACGTA CCGTGTGGTC AGCGTCCTCA CCGTCCTGCA CCAGGACTGG	300
CTGAATGGCA AGGAGTACAA GTGCAAGGTC TCCAACAAAG CCCTCCCAGC CCCCCATCGAG	360
AAAACCATCT CCAAAGCCAA AGGGCAGCCC CGAGAACAC AGGTGTACAC CCTGCC	420
CCCCGGGATG AGCTGACCAA GAACCAGGTC AGCCTGACCT GCCTGGTCAA AGGCTTCTAT	480
CCCAGCGACA TCGCCGTGGA GTGGGAGAGC AATGGGCAGC CGGAGAACAA CTACAAGACC	540
ACGCCTCCCG TGCTGGACTC CGACGGCTCC TTCTTCCTCT ACAGCAAGCT CACCGTGGAC	600
AAGAGCAGGT GGCAGCAGGG GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC	660
AACCACTACA CGCAGAAGAG CCTCTCCCTG TCTCCGGTA AAGTACCGAT CCAGAAAGTT	720

CAGGACGACA CCAAAACCTT AATTAAAACG ATCGTTACGC GTATCACGGA CATCAGTCAC	780
ACCCAGTCGG TGAGCTCTAA ACAGAAAGTT ACAGGCCCTGG ACTTCATCCC GGGTCTGCAC	840
CCGATCCTGA CCTTGTCCAA AATGGACCAG ACCCTGGCTG TATACCAGCA GATCTTAACC	900
TCCATGCCGT CCCGTAACGT TATCCAGATC TCTAACGACC TCGAGAACCT TCGCGACCTG	960
CTGCACGTGC TGGCATTCTC CAAATCCTGC CACCTGCCAT GGGCTTCAGG TCTTGAGACT	1020
CTGGACTCTC TGGGCGGGGT CCTGGAAAGCA TCCGGTTACA GCACCGAAGT TGTTGCTCTG	1080
TCCC GTCTGC AGGGTTCCCT TCAGGACATG CTTTGGCAGC TGGACCTGTC TCCGGTTGT	1140
TAATGGATCC	1150

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTATAACCTTG GGTTTAGAAC ACTGTTTGA GTGTGTACGG GTGGCACGGG TCGTGGACTT	60
GAGGACCCCC CTGGCAGTCA GAAGGAGAAG GGGGGTTTG GGTTCTGTG GGAGTACTAG	120
AGGGCCTGGG GACTCCAGTG TACGCACCAAC CACCTGCACT CGGTGCTTCT GGGACTCCAG	180
TTCAAGTTGA CCATGCACCT GCCGCACCTC CACGTATTAC GGTTCTGTGTT CGGCGCCCTC	240
CTCGTCATGT TGTCGTGCAT GGCACACCAAG TCGCAGGAGT GGCAGGACGT GGTCTGACC	300
GACTTACCGT TCCTCATGTT CACGTTCCAG AGGTTGTTTC GGGAGGGTCG GGGGTAGCTC	360
TTTTGGTAGA GGTTTCGGTT TCCCGTCGGG GCTCTTGGTG TCCACATGTG GGACGGGGT	420
AGGGCCCTAC TCGACTGGTT CTTGGTCCAG TCGGACTGGA CGGACCAAGTT TCCGAAGATA	480
GGGTCGCTGT AGCGGCACCT CACCCCTCTCG TTACCCGTGCG GCCTCTTGTGTT GATGTTCTGG	540
TGCGGAGGGC ACGACCTGAG GCTGCCGAGG AAGAAGGAGA TGTGTTCGA GTGGCACCTG	600
TTCTCGTCCA CCGTCGTCCC CTTGCAGAAG AGTACGAGGC ACTACGTACT CCGAGACGTG	660
TTGGTGATGT GCGTCTTCTC GGAGAGGGAC AGAGGGCCAT TTCATGGCTA GGTCTTCAA	720

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GTCCTGCTGT GGTTTGAA TTAATTTGC TAGCAATGCG CATAAGTGGCT GTAGTCAGTG	780
TGGGTCAAGCC ACTCGAGATT TGTCTTCAA TGTCGGACC TGAAGTAGGG CCCAGACGTG	840
GGCTAGGACT GGAACAGGTT TTACCTGGTC TGGGACCGAC ATATGGTCGT CTAGAATTGG	900
AGGTACGGCA GGGCATTGCA ATAGGTCTAG AGATTGCTGG AGCTCTTGGA AGCGCTGGAC	960
GACGTGCCACG ACCGTAAGAG GTTTAGGACG GTGGACGGTA CCCGAAGTCC AGAACTCTGA	1020
GACCTGAGAG ACCCGCCCCA GGACCTTCGT AGGCCAATGT CGTGGCTTCA ACAACGAGAC	1080
AGGGCAGACG TCCCAAGGGA AGTCCTGTAC GAAACCGTCG ACCTGGACAG AGGCCAACACA	1140
ATTACCTAGG	1150

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Protein  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /note= "Met (ATG) starts at -1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Pro Cys Pro  
1 5 10 15

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
65                   70                   75                   80

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Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
100 105 110

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
115 120 125

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
130 135 140

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
145 150 155 160

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
210 215 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys Val Pro Ile Gln Lys Val Gln  
225 230 235 240

Asp Asp Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp  
245 250 255

Ile Ser His Thr Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu  
260 265 270

Asp Phe Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp  
275 280 285

Gln Thr Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg  
290 295 300

Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu  
305 310 315 320

His Val Leu Ala Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly  
325 330 335

Leu Glu Thr Leu Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr  
340 345 350

Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp  
355 360 365

Met Leu Trp Gln Leu Asp Leu Ser Pro Gly Cys  
 370                           375

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Met = ATG"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATATGGAAC CAAAATCTGC TGACAAAACT CACACATGTC CACCTTGTCC AGCTCCGGAA	60
CTCCTGGGGG GTCCTTCAGT CTTCCCTCTTC CCCCCAAAAAC CCAAGGACAC CCTCATGATC	120
TCCCCGGACCC CTGAGGTCAC ATGCGTGGTG GTGGACGTGA GCCACGAAGA CCCTGAGGTC	180
AAGTTCAACT GGTACGTGGA CGGGGTGGAG GTGCATAATG CCAAGACAAA GCCGCGGGAG	240
GAGCAGTACA ACAGCACGTA CCGTGTGGTC AGCGTCCTCA CCGTCCTGCA CCAGGACTG	300
CTGAATGGCA AGGAGTACAA GTGCAAGGTC TCCAACAAAG CCCTCCCAGC CCCCATCGAG	360
AAAACCATCT CCAAAGCAA AGGGCAGCCC CGAGAACAC AGGTGTACAC CCTGCCCA	420
TCCCCGGATG AGCTGACCAA GAACCAAGGTC AGCCTGACCT GCCTGGTCAA AGGCTTCTAT	480
CCCAGCGACA TCGCCGTGGA GTGGGAGAGC AATGGGCAGC CGGAGAACAA CTACAAGACC	540
ACGCCTCCCG TGCTGGACTC CGACGGCTCC TTCTTCTCT ACAGCAAGCT CACCGTGGAC	600
AAGAGCAGGT GGCAGCAGGG GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC	660
AACCACTACA CGCAGAAGAG CCTCTCCCTG TCTCCGGTA AAGTACCGAT CCAGAAAGTT	720
CAGGACGACA CCAAAACCTT AATTAAAACG ATCGTTACGC GTATCACGCA CATCAGTCAC	780
ACCCAGTCGG TGAGCTCTAA ACAGAAAGTT ACAGGCCTGG ACTTCATCCC GGGTCTGCAC	840
CCGATCCTGA CCTTGTCCAA AATGGACCAAG ACCCTGGCTG TATACCAGCA GATCTTAACC	900

TCCATGCCGT CCCGTAACGT TATCCAGATC TCTAACGACC TCGAGAACCT TCGCGACCTG	960
CTGCACGTGC TGGCATTCTC CAAATCCTGC CACCTGCCAT GGGCTTCAGG TCTTGAGACT	1020
CTGGACTCTC TGGGCGGGGT CCTGGAAGCA TCCGGTTACA GCACCGAAGT TGTTGCTCTG	1080
TCCCCGTCTGC AGGGTTCCCT TCAGGACATG CTTTGGCAGC TGGACCTGTC TCCGGGTGT	1140
 TAATGGATCC	 1150

## (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTATAACCTTG GTTTTAGACG ACTGTTTGA GTGTGTACAG GTGGAACAGG TCGAGGCCTT	60
GAGGACCCCC CAGGAAGTCA GAAGGAGAAG GGGGGTTTTG GGTTCTGTG GGAGTACTAG	120
AGGGCCTGGG GACTCCAGTG TACGCACCAAC CACCTGCACT CGGTGCTTCT GGGACTCCAG	180
TTCAAGTTGA CCATGCACCT GCCGCACCTC CACGTATTAC GGTTCTGTTT CGGCGCCCTC	240
CTCGTCATGT TGTCTGTGAT GGCACACCAAG TCGCAGGAGT GGCAGGACGT GGTCTGACC	300
GACTTACCGT TCCTCATGTT CACGTTCCAG AGGTGTTTC GGGAGGGTCG GGGTAGCTC	360
TTTTGGTAGA GGTTTCGGTT TCCCGTCGGG GCTCTTGGTG TCCACATGTG GGACGGGGGT	420
AGGGCCCTAC TCGACTGGTT CTGGTCCAG TCGGACTGGA CGGACCAAGTT TCCGAAGATA	480
GGGTCCGTGT AGCGGCACCT CACCCCTCTCG TTACCCGTG GGCCTCTTGTGTT GATGTTCTGG	540
TGCGGAGGGC ACGACCTGAG GCTGCCGAGG AAGAAGGAGA TGTCTTCA GGTGGCACCTG	600
TTCTCGTCCA CCGTCGTCCC CTTGCAGAAG AGTACGAGGC ACTACGTACT CCGAGACGTG	660
TTGGTGATGT GCGTCTTCTC GGAGAGGGAC AGAGGGCCAT TTCATGGCTA GGTCTTTCAA	720
GTCCTGCTGT GGTTTGAA TTAATTTTGC TAGCAATGCG CATACTTGCT GTAGTCAGTG	780
TGGGTCAAGCC ACTCGAGATT TGTCTTCAA TGTCCGGACC TGAAGTAGGG CCCAGACGTG	840

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GGCTAGGACT GGAAACAGGTT TTACCTGGTC TGGGACCGAC ATATGGTCGT CTAGAATTGG	900
AGGTACGGCA GGGCATTGCA ATAGGTCTAG AGATTGCTGG AGCTCTTGGA AGCGCTGGAC	960
GACGTGCACG ACCGTAAGAG GTTTAGGACG GTGGACGGTA CCCGAAGTCC AGAACTCTGA	1020
GACCTGAGAG ACCCGCCCCA GGACCTTCGT AGGCCAATGT CGTGGCTTCA ACAACGAGAC	1080
AGGGCAGACG TCCCAAGGGA AGTCCTGTAC GAAACC GTCG ACCTGGACAG AGGCCAAACA	1140
<b>ATTACCTAGG</b>	<b>1150</b>

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

**(ix) FEATURE:**

(A) NAME/KEY: Protein  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /note= "Met (ATG) starts at -1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
1 5 10 15

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
65                   70                   75                   80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
100 105 110

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Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
115 120 125

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
130 135 140

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
145 150 155 160

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
210 215 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys Val Pro Ile Gln Lys Val Gln  
225 230 235 240

Asp Asp Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp  
245 250 255

Ile Ser His Thr Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu  
260 265 270

Asp Phe Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp  
275 280 285

Gln Thr Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg  
290 295 300

Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu  
305 310 315 320

His Val Leu Ala Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly  
325 330 335

Leu Glu Thr Leu Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr  
340 345 350

Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp  
355 360 365

Met Leu Trp Gln Leu Asp Leu Ser Pro Gly Cys  
370 375

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Met = ATG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CATATGGACA	AAACTCACAC	ATGTCCACCT	TGTCCAGCTC	CGGAACTCCT	GGGGGGTCCT	60
TCAGTCTTCC	TCTTCCCCCC	AAAACCCAAG	GACACCCCTCA	TGATCTCCCG	GACCCCTGAG	120
GTCACATGCG	TGGTGGTGGA	CGTGAGGCCAC	GAAGACCCCTG	AGGTCAAGTT	CAACTGGTAC	180
GTGGACGGCG	TGGAGGTGCA	TAATGCCAAG	ACAAAGCCGC	GGGAGGAGCA	GTACAACAGC	240
ACGTACCGTG	TGGTCAGCGT	CCTCACCGTC	CTGCACCAGG	ACTGGCTGAA	TGGCAAGGAG	300
TACAAGTGCA	AGGTCTCCAA	CAAAGCCCTC	CCAGCCCCCA	TCGAGAAAAAC	CATCTCCAAA	360
GCCAAAGGGC	AGCCCCGAGA	ACCACAGGTG	TACACCCCTGC	CCCCATCCCG	GGATGAGCTG	420
ACCAAGAAC	AGGTCAAGCCT	GACCTGCCTG	GTCAAAGGCT	TCTATCCCAG	CGACATCGCC	480
GTGGAGTGGG	AGAGCAATGG	GCAGCCGGAG	AACAACTACA	AGACCACGCC	TCCCGTGTG	540
GACTCCGACG	GCTCCCTCTT	CCTCTACAGC	AAGCTCACCG	TGGACAAGAG	CAGGTGGCAG	600
CAGGGGAACG	TCTTCTCATG	CTCCGTGATG	CATGAGGCTC	TGCACAACCA	CTACACGCAG	660
AAGAGCCTCT	CCCTGTCTCC	GGGTAAAGTA	CCGATCCAGA	AAGTTCAGGA	CGACACCAAA	720
ACCTTAATT	AAACGATCGT	TACGGGTATC	AACGACATCA	GTCACACCCA	GTCGGTGAGC	780
TCTAACACAGA	AAGTTACAGG	CCTGGACTTC	ATCCCGGGTC	TGCACCCGAT	CCTGACCTTG	840
TCCAAAATGG	ACCAGACCCCT	GGCTGTATAAC	CAGCAGATCT	TAACCTCCAT	GCCGTCCCGT	900
AACGTTATCC	AGATCTCTAA	CGACCTCGAG	AACCTTCGCG	ACCTGCTGCA	CCTGCTGGCA	960
TTCTCCAAAT	CCTGCCACCT	GCCATGGGCT	TCAGGTCTTG	AGACTCTGGA	CTCTCTGGGC	1020

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GGGGTCTGG AAGCATCCGG TTACAGCACC GAAGTTGTTG CTCTGTCCCC TCTGCAGGGT	1080
TCCCTTCAGG ACATGCTTTG GCAGCTGGAC CTGTCTCCGG GTTGTAAATG GATCC	1135

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTATAACCTGT TTTGAGTGTG TACAGGTGGA ACAGGTCGAG GCCTTGAGGA CCCCCCAGGA	60
AGTCAGAAGG AGAAGGGGGG TTTTGGGTTT CTGTGGGAGT ACTAGAGGGC CTGGGGACTC	120
CAGTGTACGC ACCACCACCT GCACTCGGTG CTTCTGGGAC TCCAGTTCAA GTTGACCATG	180
CACCTGCCGC ACCTCCACGT ATTACGGTTT TGTTTCGGCG CCCTCCTCGT CATGTTGTCG	240
TGCATGGCAC ACCAGTCGCA GGAGTGGCAG GACGTGGTCC TGACCGACTT ACCGTTCCCTC	300
ATGTTCACGT TCCAGAGGTT GTTTGGGAG GGTCGGGGGT AGCTTTTG GTAGAGGTTT	360
CGGTTCCCG TCAGGGCTCT TGGTGTCCAC ATGTGGGACG GGGTAGGGC CCTACTCGAC	420
TGGTTCTTGG TCCAGTCGGA CTGGACGGAC CAGTTCCGA AGATAGGGTC GCTGTAGCGG	480
CACCTCACCC TCTCGTTACC CGTCGGCCTC TTGTTGATGT TCTGGTGCAG AGGGCACCGAC	540
CTGAGGCTGC CGAGGAAGAA GGAGATGTCG TTGAGTGGC ACCTGTTCTC GTCCACCGTC	600
GTCCCCTTGC AGAAGAGTAC GAGGCACTAC GTACTCCGAG ACGTGGTGGT GATGTGGTC	660
TTCTCGGAGA GGGACAGAGG CCCATTTCAT GGCTAGGTCT TTCAAGTCCT GCTGTGGTTT	720
TGGAATTAAT TTGCTAGCA ATGGCCTAG TTGCTGTAGT CAGTGTGGGT CAGCCACTCG	780
AGATTTGTCT TTCAATGTCC GGACTCTGAAG TAGGGCCAG ACGTGGGCTA GGACTGGAAC	840
AGGTTTTACC TGGTCTGGGA CCGACATATG GTCTGCTAGA ATTGGAGGTA CGGCAGGGCA	900
TTGCAATAGG TCTAGAGATT GCTGGAGCTC TTGGAAGGGC TGGACGGACGT GCACGACCGT	960
AAGAGGTTTA GGACGGTGGA CGGTACCCGA AGTCCAGAAC TCTGAGACCT GAGAGACCCG	1020
CCCCAGGACC TTGCTAGGCC AATGTCGTGG CTTCAACAAC GAGACAGGGC AGACGTCCCA	1080

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AGGGAAAGTCC TGTACGAAAC CGTCGACCTG GACAGAGGCC CAACAATTAC CTAGG

1135

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

## (ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met (ATG) starts at -1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu  
1 5 10 15

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
35 40 45

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
65 70 75 80

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
100 105 110

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
145 150 155 160

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Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
															165
															170
															175
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr
															180
															185
															190
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val
															195
															200
															205
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu
															210
															215
															220
Ser	Pro	Gly	Lys	Val	Pro	Ile	Gln	Lys	Val	Gln	Asp	Asp	Thr	Lys	Thr
															225
															230
															235
															240
Leu	Ile	Lys	Thr	Ile	Val	Thr	Arg	Ile	Asn	Asp	Ile	Ser	His	Thr	Gln
															245
															250
															255
Ser	Val	Ser	Ser	Lys	Gln	Lys	Val	Thr	Gly	Leu	Asp	Phe	Ile	Pro	Gly
															260
															265
															270
Leu	His	Pro	Ile	Leu	Thr	Leu	Ser	Lys	Met	Asp	Gln	Thr	Leu	Ala	Val
															275
															280
															285
Tyr	Gln	Gln	Ile	Leu	Thr	Ser	Met	Pro	Ser	Arg	Asn	Val	Ile	Gln	Ile
															290
															295
															300
Ser	Asn	Asp	Leu	Glu	Asn	Leu	Arg	Asp	Leu	Leu	His	Val	Leu	Ala	Phe
															305
															310
															315
															320
Ser	Lys	Ser	Cys	His	Leu	Pro	Trp	Ala	Ser	Gly	Leu	Glu	Thr	Leu	Asp
															325
															330
															335
Ser	Leu	Gly	Gly	Val	Leu	Glu	Ala	Ser	Gly	Tyr	Ser	Thr	Glu	Val	Val
															340
															345
															350
Ala	Leu	Ser	Arg	Leu	Gln	Gly	Ser	Leu	Gln	Asp	Met	Leu	Trp	Gln	Leu
															355
															360
															365
Asp	Leu	Ser	Pro	Gly	Cys										
															370

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Met = ATG"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATATGGACA	AAACTCACAC	ATGCCAACCG	TGCCAGCTC	CGGAACTCGA	AGGTGGTCCG	60
TCAGTCTTCC	TCTTCCCCCC	AAAACCAAG	GACACCCTCA	TGATCTCCG	GACCCCTGAG	120
GTCACATGCG	TGGTGGTGG	CGTGAGCCAC	GAAGACCTG	AGGTCAAGTT	CAAATGGTAC	180
GTGGACGGCG	TGGAGGTGCA	TAATGCCAAG	ACAAAGCCGC	GGGAGGAGCA	GTACAACAGC	240
ACGTACCGTG	TGGTCAGCGT	CCTCACCGTC	CTGCACCAAGG	ACTGGCTGAA	TGGCAAAGCT	300
TACGCATGCG	CGGTCTCCAA	CAAAGCCCTC	CCAGCCCCCA	TCGAGAAAAC	CATCTCCAAA	360
GCCAAAGGGC	AGCCCCGAGA	ACCACAGGTG	TACACCCCTGC	CCCCATCCCG	GGATGAGCTG	420
ACCAAGAAC	AGGTCAGCCT	GACCTGCCTG	GTCAAAGGCT	TCTATCCCAG	CGACATCGCC	480
GTGGAGTGGG	AGAGCAATGG	GCAGCCGGAG	AACAAC TACA	AGACCACGCC	TCCCGTGCTG	540
GACTCCGACG	GCTCCTTCTT	CCTCTACAGC	AAGCTCACCG	TGGACAAGAG	CAGGTGGCAG	600
CAGGGGAACG	TCTTCTCATG	CTCCGTGATG	CATGAGGCTC	TGCACAAACCA	CTACACGCAG	660
AAGAGCCTCT	CCCTGTCTCC	GGGTAAAGTA	CCGATCCAGA	AAGTTCAAGGA	CGACACCCAA	720
ACCTTAATTA	AAACGATCGT	TACCGGTATC	AACGACATCA	GTCACACCCCA	GTCGGTGAGC	780
TCTAACAGA	AAGTTACAGG	CCTGGACTTC	ATCCC GGTC	TGCACCCGAT	CCTGACCTTG	840
TCCAAAATGG	ACCAGACCCCT	GGCTGTATAAC	CAGCAGATCT	TAACCTCCAT	GCCGTCCCGT	900
AACGTTATCC	AGATCTCTAA	CGACCTCGAG	AACCTTCGCG	ACCTGCTGCA	CGTGCTGGCA	960
TTCTCCAAAT	CCTGCCACCT	GCCATGGGCT	TCAGGTCTTG	AGACTCTGGA	CTCTCTGGGC	1020
GGGGTCTGG	AAGCATCCGG	TTACAGCACC	GAAGTTGTTG	CTCTGTCCCG	TCTGCAGGGT	1080
TCCCTTCAGG	ACATGCTTTC	GCAGCTGGAC	CTGTCTCCGG	GTTGTTAATG	GATCC	1135

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## (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTATAACCTGT TTTGAGTGTG TACGGGTGGC ACGGGTCGAG GCCTTGAGCT TCCACCAGGC	60
AGTCAGAACGG AGAACGGGGGG TTTTGGGTTTC CTGTGGGAGT ACTAGAGGGC CTGGGGACTC	120
CAGTGTACGC ACCACCACCT GCACTCGGTG CTTCTGGGAC TCCAGTTCAA GTTGACCATG	180
CACCTGCCGC ACCTCCACGT ATTACGGTTTC TGTTTCGGCG CCCTCCTCGT CATGTTGTCG	240
TGCATGGCAC ACCAGTCGCA GGAGTGGCAG GACGTGGTCC TGACCGACTT ACCGTTTCGA	300
ATGCGTACGC GCCAGAGGTT GTTTCGGGAG GGTCGGGGGT AGCTCTTTTG GTAGAGGTTT	360
CGGTTTCCCG TCGGGGCTCT TGGTGTCCAC ATGTGGGACG GGGTAGGGC CCTACTCGAC	420
TGGTTCTTGG TCCAGTCGGA CTGGACGGAC CAGTTTCCGA AGATAGGGTC GCTGTAGCGG	480
CACCTCACCC TCTCGTTACC CGTCGGCCTC TTGTTGATGT TCTGGTGGCG AGGGCACGAC	540
CTGAGGCTGC CGAGGAAGAA GGAGATGTCG TTGAGTGGC ACCTGTTCTC GTCCACCGTC	600
GTCCCCCTTGC AGAAAGAGTAC GAGGCACTAC GTACTCCGAG ACGTGTGGT GATGTGGC	660
TTCTCGGAGA GGGACAGAGG CCCATTTCAT GGCTAGGTCT TTCAAGTCCT GCTGTGGTTT	720
TGGAATTAAAT TTTGCTAGCA ATGCGCATAG TTGCTGTAGT CAGTGTGGGT CAGCCACTCG	780
AGATTTGTCT TTCAATGTCC GGACCTGAAG TAGGGCCCAG ACGTGGGCTA GGACTGGAAC	840
AGGTTTTTACCG TGGCTGGGA CCGACATATG GTCGTCTAGA ATTGGAGGTA CGGCAGGGCA	900
TTGCAATAGG TCTAGAGATT GCTGGAGCTC TTGGAAGCGC TGGACGACGT GCACGACCGT	960
AAGAGGTTTA GGACGGTGGA CGGTACCCGA AGTCCAGAAC TCTGAGACCT GAGAGACCCG	1020
CCCCAGGACC TTGCTAGGCC AATGTCGTGG CTTCAACAAC GAGACAGGGC AGACGTCCCCA	1080
AGGGAAGTCC TGTACGAAAC CGTCGACCTG GACAGAGGCC CAACAATTAC CTAGG	1135

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met (ATG) starts at -1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Glu  
1 5 10 15

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
35 40 45

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu  
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr  
65 70 75 80

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
85 90 95

Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro  
100 105 110

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val  
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
165 170 175

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Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr  
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
210 215 220

Ser Pro Gly Lys Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr  
225 230 235 240

Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln  
245 250 255

Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly  
260 265 270

Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val  
275 280 285

Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile  
290 295 300

Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe  
305 310 315 320

Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp  
325 330 335

Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val  
340 345 350

Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu  
355 360 365

Asp Leu Ser Pro Gly Cys  
370

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CLAIMS

1. A protein having a formula selected from  
the group consisting of: R<sub>1</sub> - R<sub>2</sub> and R<sub>1</sub> - L - R<sub>2</sub>, wherein  
5 R<sub>1</sub> is a Fc protein or analog thereof, R<sub>2</sub> is an OB protein  
or analog thereof, and L is a linker.

2. The protein according to claim 1, where  
in the Fc, analog or derivative is selected from the  
10 group consisting of:

- (a) the Fc amino acid sequences as set forth  
in SEQ. ID. NOS.: 9, 12, 15 and 18;
- (b) the amino acid sequence of subpart (a)  
having a different amino acid substituted or  
15 deleted in one or more of the following positions  
(using the numbering according to SEQ. ID. NO. 9):
  - (i) one or more cysteine residues  
replace by an alanine or serine residue;
  - (ii) one or more tyrosine residues  
replaced by a phenylalanine residue;
  - (iii) the amino acid at position 5  
replaced with an alanine;
  - (iv) the amino acid at position 20  
replaced with glutamate;
  - 25 (v) the amino acid at position 103  
replaced with an alanine;
  - (vi) the amino acid at position 105  
replaced with an alanine;
  - (vii) the amino acid at position 107  
replaced with an alanine;
  - (viii) the amino acids at positions 1,  
30 2, 3, 4, or 5 deleted;
  - (ix) one or more residues replaced  
or deleted to ablate the Fc receptor binding site;

(x) one or more residues replaced or deleted to ablate the complement (C1q) binding site; and

(xi) a combination of subparts i-x;

5 (c) the amino acid sequence of subparts (a) or (b) having a methionyl residue at the N-terminus;

10 (d) the Fc protein, analog or derivative of any of subparts (a) through (c) comprised of a chemical moiety connected to the protein moiety;

(e) a derivative of subpart (d) wherein said chemical moiety is a water soluble polymer moiety;

15 (f) a derivative of subpart (e) wherein said water soluble polymer moiety is polyethylene glycol;

(g) A derivative of subpart (e) wherein said water soluble polymer moiety is a polyamino acid moiety; and

20 (h) a derivative of subpart (e) wherein said water soluble polymer moiety is attached at solely the N-terminus of said protein moiety.

3. The protein according to claim 1, wherein the OB protein, analog or derivative is selected from  
25 the group consisting of:

(a) the amino acid sequence 1-146 as set forth in SEQ. ID. NO. 3 or SEQ. ID. NO. 6;

30 (b) the amino acid sequence 1-146 as set forth in SEQ. ID. NO. 6 having a lysine residue at position 35 and an isoleucine residue at position 74;

35 (c) the amino acid sequence of subpart (b) having a different amino acid substituted in one or more of the following positions (using the numbering according to SEQ. ID. NO. 6): 4, 8, 32,

33, 35, 48, 50, 53, 60, 64, 66, 67, 68, 71, 74, 77,  
78, 89, 97, 100, 102, 105, 106, 107, 108, 111,  
112, 118, 136, 138, 142, and 145;

5

(d) the amino acid sequence of subparts (a),  
(b) or (c) optionally lacking a glutaminyl residue  
at position 28;

10

(e) the amino acid sequence of subparts (a),  
(b), (c), or (d) having a methionyl residue at the  
N-terminus.

15

(f) a truncated OB protein analog selected  
from among: (using the numbering of SEQ. ID. NO. 6  
having a lysine residue at position 35, and an  
isoleucine residue at position 74):

20

(i) amino acids 98-146  
(ii) amino acids 1-32  
(iii) amino acids 40-116  
(iv) amino acids 1-99 and 112-146  
(v) amino acids 1-99 and 112-146 having  
one or more of amino acids 100-111 sequentially  
placed between amino acids 99 and 112; and,

25

(vi) the truncated OB analog of subpart  
(f)(i) having one or more of amino acids 100, 102,  
105, 106, 107, 108, 111, 112, 118, 136, 138, 142,  
and 145 substituted with another amino acid;

30

(vii) the truncated analog of subpart  
(f)(ii) having one or more of amino acids 4, 8 and  
32 substituted with another amino acid;  
(viii) the truncated analog of subpart  
(f)(iii) having one or more of amino acids 50, 53,  
60, 64, 66, 67, 68, 71, 74, 77, 78, 89, 97, 100,  
102, 105, 106, 107, 108, 111 and 112 replaced with  
another amino acid;

(ix) the truncated analog of subpart  
(f)(iv) having one or more of amino acids 4, 8, 32,

33, 35, 48, 50, 53, 60, 64, 66, 67, 68, 71, 74, 77,  
78, 89, 97, 112, 118, 136, 138, 142, and 145  
replaced with another amino acid;

(x) the truncated analog of subpart

5 (f) (v) having one or more of amino acids 4, 8, 32,  
33, 35, 48, 50, 53, 60, 64, 66, 67, 68, 71, 74,  
77, 78, 89, 97, 100, 102, 105, 106, 107, 108, 111,  
112, 118, 136, 138, 142, and 145 replaced with  
another amino acid;

10 (xi) the truncated analog of any of  
subparts (f) (i)-(x) having an N-terminal methionyl  
residue;

15 (g) the OB protein or analog derivative of  
any of subparts (a) through (f) comprised of a  
chemical moiety connected to the protein moiety;

(h) a derivative of subpart (g) wherein said  
chemical moiety is a water soluble polymer moiety;

20 (i) a derivative of subpart (h) wherein said  
water soluble polymer moiety is polyethylene  
glycol;

(j) A derivative of subpart (h) wherein said  
water soluble polymer moiety is a polyamino acid  
moiety; and

25 (k) a derivative of subpart (h) wherein said  
water soluble polymer moiety is attached at solely  
the N-terminus of said protein moiety.

4. The protein of claim 1 wherein the linker  
sequence is one or more amino acids selected from the  
30 group consisting of: Glycine, Asparagine, Serine,  
Threonine and Alanine.

5. The protein of claim 1 wherein the linker  
is selected from the group consisting of:

35 (a) ala, ala, ala;  
(b) ala, ala, ala, ala;

(c) ala, ala, ala, ala, ala;  
(d) gly, gly;  
(e) gly, gly, gly;  
(f) gly, gly, gly, gly, gly;  
5 (g) gly, gly, gly, gly, gly, gly, gly;  
(h) gly-pro-gly;  
(i) gly, gly, pro, gly, gly;  
(j) chemical moiety; and  
(k) any combination of subparts (a)  
10 through (j).

6. A fusion protein comprising a Fc protein, analog or derivative thereof, fused to the N-terminus of an OB protein, analog or derivative thereof.

7. A nucleic acid sequence encoding for a protein having the formula selected from the group consisting of: R<sub>1</sub> - R<sub>2</sub> and R<sub>1</sub> - L - R<sub>2</sub>, wherein R<sub>1</sub> is a Fc protein or analog thereof, R<sub>2</sub> is an OB protein or analog thereof, and L is a linker.

8. The nucleic acid sequence according to claim 7 encoding for a protein having a Fc, analog or derivative portion selected from the group consisting of:

(a) the Fc amino acid sequences as set forth in SEQ. ID. NOS.: 9, 12, 15 and 18;  
30 (b) the amino acid sequence of subpart (a) having a different amino acid substituted or deleted in one or more of the following positions (using the numbering according to SEQ. ID. NO. 9):  
(i) one or more cysteine residues replace by an alanine or serine residue;

- (ii) one or more tyrosine residues replaced by a phenylalanine residue;
- (iii) the amino acid at position 5 replaced with an alanine;
- 5 (iv) the amino acid at position 20 replaced with glutamate;
- (v) the amino acid at position 103 replaced with an alanine;
- 10 (vi) the amino acid at position 105 replaced with an alanine;
- (vii) the amino acid at position 107 replaced with an alanine;
- (viii) the amino acids at positions 1, 2, 3, 4, or 5 deleted;
- 15 (ix) one or more residues replaced or deleted to ablate the Fc receptor binding site;
- (x) one or more residues replaced or deleted to ablate the complement (C1q) binding site; and
- 20 (xi) a combination of subparts i-x;
- (c) the amino acid sequence of subparts (a) or (b) having a methionyl residue at the N-terminus;
- (d) the Fc protein, analog or derivative of any of subparts (a) through (c) comprised of a chemical moiety connected to the protein moiety;
- 25 (e) a derivative of subpart (d) wherein said chemical moiety is a water soluble polymer moiety;
- (f) a derivative of subpart (e) wherein said water soluble polymer moiety is polyethylene glycol;
- 30 (g) A derivative of subpart (e) wherein said water soluble polymer moiety is a polyamino acid moiety; and

(h) a derivative of subpart (e) wherein said water soluble polymer moiety is attached at solely the N-terminus of said protein moiety.

5           9. The nucleic acid sequence according to claim 7 encoding for a protein having an OB protein, analog or derivative portion selected from the group consisting of:

10           (a) the amino acid sequence 1-146 as set forth in SEQ. ID. NO. 3 or SEQ. ID. NO. 6;

              (b) the amino acid sequence 1-146 as set forth in SEQ. ID. NO. 6 having a lysine residue at position 35 and an isoleucine residue at position 74;

15           (c) the amino acid sequence of subpart (b) having a different amino acid substituted in one or more of the following positions (using the numbering according to SEQ. ID. NO. 6): 4, 8, 32, 33, 35, 48, 50, 53, 60, 64, 66, 67, 68, 71, 74, 77, 78, 89, 97, 100, 102, 105, 106, 107, 108, 111, 20        112, 118, 136, 138, 142, and 145;

              (d) the amino acid sequence of subparts (a), (b) or (c) optionally lacking a glutamyl residue at position 28;

25           (e) the amino acid sequence of subparts (a), (b), (c), or (d) having a methionyl residue at the N terminus.

              (f) a truncated OB protein analog selected from among: (using the numbering of SEQ. ID. NO. 6 having a lysine residue at position 35, and an isoleucine residue at position 74):

              (i) amino acids 98-146

              (ii) amino acids 1-32

              (iii) amino acids 40-116

35           (iv) amino acids 1-99 and 112-146

(v) amino acids 1-99 and 112-146 having one or more of amino acids 100-111 sequentially placed between amino acids 99 and 112; and,

(vi) the truncated OB analog of subpart (f)(i) having one or more of amino acids 100, 102, 105, 106, 107, 108, 111, 112, 118, 136, 138, 142, and 145 substituted with another amino acid;

(vii) the truncated analog of subpart (f)(ii) having one or more of amino acids 4, 8 and 32 substituted with another amino acid;

(viii) the truncated analog of subpart (f)(iii) having one or more of amino acids 50, 53, 60, 64, 66, 67, 68, 71, 74, 77, 78, 89, 97, 100, 102, 105, 106, 107, 108, 111 and 112 replaced with another amino acid;

(ix) the truncated analog of subpart (f)(iv) having one or more of amino acids 4, 8, 32, 33, 35, 48, 50, 53, 60, 64, 66, 67, 68, 71, 74, 77, 78, 89, 97, 112, 118, 136, 138, 142, and 145 replaced with another amino acid;

(x) the truncated analog of subpart (f)(v) having one or more of amino acids 4, 8, 32, 33, 35, 48, 50, 53, 60, 64, 66, 67, 68, 71, 74, 77, 78, 89, 97, 100, 102, 105, 106, 107, 108, 111, 112, 118, 136, 138, 142, and 145 replaced with another amino acid;

(xi) the truncated analog of any of subparts (f)(i)-(x) having an N-terminal methionyl residue;

(g) the OB protein or analog derivative of any of subparts (a) through (f) comprised of a chemical moiety connected to the protein moiety;

(h) a derivative of subpart (g) wherein said chemical moiety is a water soluble polymer moiety;

(i) a derivative of subpart (h) wherein said water soluble polymer moiety is polyethylene glycol;

5 (j) A derivative of subpart (h) wherein said water soluble polymer moiety is a polyamino acid moiety; and

(k) a derivative of subpart (h) wherein said water soluble polymer moiety is attached at solely the N-terminus of said protein moiety.

10

10. The nucleic acid sequence of claim 7 encoding for a protein with a linker sequence of one or more amino acids selected from the group consisting of: Gly, Asn, Ser, Thr and Ala.

15

11. The nucleic acid sequence of claim 7 encoding for a protein with a linker selected from the group consisting of:

- (a) ala, ala, ala;
- 20 (b) ala, ala, ala, ala;
- (c) ala, ala, ala, ala, ala;
- (d) gly, gly;
- (e) gly, gly, gly;
- (f) gly, gly, gly, gly, gly;
- 25 (g) gly, gly, gly, gly, gly, gly, gly;
- (h) gly-pro-gly;
- (i) gly, gly, pro, gly, gly;
- (j) a chemical moiety; and
- (k) any combination of subparts (a)

30 through (j).

12. A nucleic acid sequence encoding for a fusion protein having a Fc protein, analog or derivative thereof, fused to the N-terminus of an OB protein, 35 analog or derivative thereof.

13. A vector containing a nucleic acid sequence according to claims 7 or 12.

14. The vector of claim 13 wherein the vector 5 is pAMG21 and the nucleic acid sequence according to claims 7 or 12.

15. A prokaryotic or eukaryotic host cell containing the vector of claim 13.

10

16. A process for producing a protein of claims 1 or 6 comprising the steps of culturing, under suitable conditions, the host cell of claim 15, and isolating the protein produced.

15

17. The process of claim 16 further comprising the step of purifying the protein produced.

20

18. A pharmaceutical composition comprising an effective amount of a protein according to claims 1 or 6, in a pharmaceutically acceptable diluent, adjuvant or carrier.

25

19. A method of treatment of a disorder selected from the group consisting of excess weight, diabetes, high blood lipid level, arterial sclerosis, arterial plaque, the reduction or prevention of gall stones formation, insufficient lean tissue mass, insufficient sensitivity to insulin, and stroke, wherein 30 the method consists of administering a therapeutically effective amount of the protein according to claims 1 or 6.

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**FIG 1A**

249 -+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 CTC CCTGCCGTCCCCAGAACGTTCTTCAGATCGCATACGACCCCTCGAGAACCTTCGGCGACT  
 308 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 GAGGGACGGCAGGGTCTTGCAAGGAAGTCTAGCGATTGCTGGAGGCTCTTGAAAGGCCTGGA  
 S L P S Q N V L Q I A N D L E N L R D L -  
 L H L A F S K S C S L P Q T S G L Q K -  
 ACCGGAAATCCCTTGGACGGGGTCCCTGGAAAGCATTCCCTGTACAGCACCGAAGTTGTTGCTCT  
 369 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 TGGCCCTTAGGGACCTGGCCAGGACCTTGTAGGGACATGTCTGGCTCAACAAACGAGA  
 P E S L D G V L E A S L Y S T E V V A L -  
 / 2 / 4  
 GTCCCGTCTGCAGGGTTCCCTTCAGGACATCCTTCAGCAGCTGGACGTTCTCCGGAAATG  
 429 +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 CAGGGCAGACGGTCCCAAGGGAAAGTCCTGTAGGAAGTCTGACCTGCAAAAGAGGGCTTAC  
 S R L Q G S L Q D I L Q Q L D V S P E C -  
 TTAATGGATCC  
 489 -+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 ATTACCTAGG

FIG 1B

FIG 2A

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FIG 2B

## FIG 3A-1

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CATATGGAACCCAAATCTTGTGACAAAACACTCACACATGCCAACCGTGGCCAGGCACCTGAA	60
1 ---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+	
GTATAACCTTGGTTAGAACACTGTTTGAGTGTGTACGGTGGACGGTGGTGTGGACTT	
M E P K S C D K T H T C P P C P A P E -	
CTCCTGGGGACCGTCAGTCAGTCTTCCTCTTCCCCAAACCCAAAGGACACCCCTCATGATC	120
61 ---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+	
GAGGACCCCCCTGGCAGTCAGTCAAGGAGAACGGAGAACGGGTTTGGGTCTGGAGTAGCTAG	
L L G G P S V F L F P P K P K D T L M I -	
TCCCGGACCCCTGAGGTACATGGCTGGTGGACGGTGGACGGCACGAAAGACCCCTGAGGTC	180
121 ---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+	
AGGGCCTGGGACTCCAGTGTACGGCACCCACCTGCACACTCGGTCTGGACTTCCAG	
S R T P E V T C V V D V S H E D P E V -	
AAGTTCAACTGGTACGTGGACGGCGTGGAGGGCATATAATGCCAAGACAAAGCCGGGAG	240
181 ---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+	
TTCAGTTGACCATGCCCTGGCGCACCTCACGTATTACGGTCTGGTCTGGCCCTC	
K F N W Y V D G V E V H N A K T K P R E -	

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GAGCAGTACACAGCACGTACCGTGTGGTCAGGGTCCACCGTCTGCACCGACTGG  
 241 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 300  
 CTCGTCATGTTGTCGTGCATGGCACACCAAGTCGCAGGAGTGGCAGGAACGTCCTGACC

E Q Y N S T Y R V V S V L T V L H Q D W -  
 301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360  
 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAAACAAGGCCCTCCCAGCCCCATCGAG  
 GACTTACCGTTCTCATGTTCACGTTCAAGGGTTCAGAGGTTGGGGAGGGTCTGGGGTAGCTC

L N G K E Y K C K V S N K A L P A P I E -  
 361 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 420  
 AAAACCATCTCCAAGGCCAAGGGCAGCCCCGAGAACCAACAGGTGTACACCCCTGCCCTCA  
 TTTGGTAGAGGTTTCGGTTTCCCGTCCGGCTCTGGTGTCCACATGTGGGACGGGGT

K T I S K A K G Q P R E P Q V Y T L P P -  
 421 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480  
 TCCCGGGATGAGCTGACCAAGAACCGAGTCAGCCTGACCTGCTGGTCAAAGGCTTCTAT  
 AGGGCCCTACTCGACTGGTTCTGGTCAAGTCGGACTGGACCGAGCTCCGAAGATA

S R D E L T K N Q V S L T C L V K G F Y -  
 481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540  
 CCCAGGGACATCGCCGTGGAGGTGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACC  
 GGGTCGCTGTAGCGGGCACCTCACCCCTCTCGTTACCCGTCGCTGGCCTCTGGTGTCTG

FIG 3A-2

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## FIG 3B-1

P S D I A V E W E S N G Q P E N N Y K T -  
 ACGCCTCCCGTGGACTCCGACGGCTCCTTCTTACAGCAAGCTCACCGTGGAC  
 541 ---+---+---+---+---+---+---+---+---+---+ 600  
 TCGGGAGGGCACGACCTGAGGCTGCCGAGGAAGGAGATGTCGTTGAGTGGCACCTG  
  
 T P P V L D S D G S F F L Y S K L T V D -  
 AAGGAGGTGGCAGCAGGGAAACGCTCTCATGCTCCGTGATGGCATGGGCTCTGCAC  
 601 ---+---+---+---+---+---+---+---+---+---+ 660  
 TTCTCGTCCACCGTGTCCCCCTGGAGAAGAGTACGAGGGCACTACGTTACTCCGAGACGTTG  
  
 K S R W Q Q N V F S C S V M H E A L H -  
 AACCACTACACGCAGAAGAGCCCTCTCCCTGTCCTCGGGTAAAGTACCGATCCAGAAAGTT  
 661 ---+---+---+---+---+---+---+---+---+---+ 720  
 TTGGTGATGTGGTCTTCTGGAGAGGGACAGAGGCCATTTCATGGCTAGGTCTTTCAA  
  
 N H Y T Q K S L S P G K V P I Q K V -  
 CAGGACGACACCAAAACCTTAATTAAACGATCGTTACGGTATCAACGACATCAGTCAC  
 721 ---+---+---+---+---+---+---+---+---+---+ 780  
 GTCCCTGCTGGTTGGAAATTAAATTGGCTAGCAATGGCATAGTTGCTGTAGTCAGTGTG  
  
 Q D D T K T L I K T I V T R I N D I S H -

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ACCCAGTGGTGAACGAAAGTTAACAGAAGCTTCATCCGGGTGGACTTCATCCGGGTCTGCAC  
 781 - - - + - - + - - + - - + - - + - - + - - + - - + - - + - - + 840  
 TGGGTCAAGCCACTCGAGATTGTCTTCAATGTCCGGACCTGAAAGTAGGGCCAGACGTTG  
  
 T Q S V S S K Q K V T G L D F I P G L H -  
  
 CCGATCCTGACCTTGTCCAAATGGACCAGACCCCTGGCTGTATACCAGCAGATCTTAACC  
 841 - - - + - - + - - + - - + - - + - - + - - + - - + - - + - - + 900  
 GGCTAGGACTGGAACAGGTTTACCTGGCTGGACCATATGGTGTCTAGAATTGG  
  
 P I L T L S K M D Q T L A V Y Q Q I L T -  
  
 TCCATGCCGTCGGTAACGTTATCCAGATCTCTAACGACCTCTGGAGAACCTTCGCCGACCTG  
 901 - - - + - - + - - + - - + - - + - - + - - + - - + - - + - - + 960  
 AGGTACGGCAGGGCATTGCAATAAGGTCTAGAGATTGCTGGAGCTCTGGAAAGGGCTGGAC  
  
 S M P S R N V I Q I S N D L E N L R D L -  
  
 CTGGCACGTGGCATTCTCCAATCTGCCACCTGGCCATGGGCTTCAGGTCTTGAGACT  
 961 - - - + - - + - - + - - + - - + - - + - - + - - + - - + 1020  
 GACGTGCACGGTAAGAGGGTTAGGACGGTGGACGGTACCCGAAGTCCAGAACCTCTGA  
  
 L H V L A F S K S C H L P W A S G L E T -  
  
 CTGGACTCTGGCGGGGTCTGGAAAGCATCCGGTTACAGGACCCGAAGTTGGCTCTG  
 1021 - - - + - - + - - + - - + - - + - - + - - + - - + - - + 1080  
 GACCTGAGAGACCCGCCAGGACCTTCGTAGGCCAATGTCTGGCTTCAACACGAGAC  
  
 L D S L G G V L E A S G Y S T E V V A L -

FIG 3B-2

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**FIG 3C**

1081	<pre> TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGGTCTCCGGTTGT AGGGCAGACGTCCAAAGGAAAGTCCGTACGAAACCGTCGACTGGACAGGGCCAAACA </pre>	<pre> S R L Q G S L Q D M L W Q L D L S P G C - </pre>
------	---	--

## FIG 4A-1

1 0 / 2 4

1    CATATGGAACCAAAATCTGGCTGACAAA 60    ACTCACACATGTCCACCTTGTCCAGCTCCGGAA GTATACCTGGTTTAGACCGACTGTTGAGTGTACAGGTGGAACAGGTGAGGCCTT	M E P K S A D K T H T C P P C P A P E -  61    CTCCTGGGGTCCCTCAGTCTTCCTCTTCCCCAAA GAGGACCCCCAGGAAGTCAGAACGGAGAACGGGGTTT L L G G P S V F L F P P K P K D T L M I -	120    +-----+ +-----+ +-----+ +-----+ TCCCGGACCCCTGAGGTACATGCCGTGGTGGACGTGAGCCACGGAAAGACCCCTCATGATC AGGGCCTGGGACTCCAGTGTACCGACCACCTGCACTCGTGC S R T P E V T C V V D V S H E D P E V -	181    +-----+ +-----+ +-----+ +-----+ AAGTTCAAACGGTACGGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAG TTCAAGTTGACCATGCAACCTGCCACCTCCACGTATTACGGTTCTGGGACTCCAG K F N W Y V D G V E V H N A K T K P R E -
--	---	---	---

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FIG 4A-2

FIG 4B-1

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ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCGGGCTGGCAC  
 781 ---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 840  
 TGGGTCAAGCCACTCGGAGATTGTCTTCAATGTCCGGACCTGAAGTAGGGCCCCAGACGTC  
  
 T Q S V S S K Q K V T G L D F I P G L H -  
  
 CCGATCCTGACCTTGTCCAAAATGGACCCAGACCCCTGGCTGTATAACCAGCAGATCTTAACC  
 841 ---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 900  
 GGCTAGGACTTGGAACAGGGTTAACCTGGTCTGGGACCCACATATGGTCGTAGAATTGG  
  
 P I L T L S K M D Q T L A V Y Q Q I L T -  
  
 TCCATGCCGTCCCGTAAACGTTATCCAGATCTTAACGACCTCGAGAACCTTCGGACCTG  
 901 ---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 960  
 AGGTACGGCAGGGCATTTGCAAATAGGTCTAGAGATTGGCTGGAGCTCTTGGAAAGGGCTGGAC  
  
 S M P S R N V I Q I S N D L E N L R D L -  
  
 CTGCACGTGCTGGCATTCTCCAATCCTGCCACCTGCCATGGCATGGCTTCAGGTCTTGAGACT  
 961 ---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 1020  
 GACGTGCACGACCGTTAGGCTTAAGGGTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA  
  
 L H V L A F S K S C H L P W A S G L E T -  
  
 CTGGACTCTGGGGGGTCTGGAAAGGCATCGGGTTACAGGCACCGAAGTTGCTCTG  
 1021 ---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 1080  
 GACCTGAGAGACCCCCAGGGACCTTCGTAGGCCAATGTCGTGGCTTCACAAACGAGAC  
  
 L D S L G V L E A S G Y S T E V V A L -

FIG 4B-2

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FIG 4C

FIG 5A-1

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241	ACGTACCGTGTGGTCAAGCGTCCTCACCGTCCCTGACCAGGACTGGCTGAATGGCAAGGAG	300
	TGCATGGCACACCAGTCGGCAGGAGTGGCAGGGACGTGGTCCCTGACCGACTAACCGTTCCCTC	
	T Y R V V S V L T V L H Q D W L N G K E -	
301	TACAAGTCAAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAACCATCTCCAAA	360
	ATGTTCACGGTCCAGAGGTTGTTTCGGGAGGGTCCGGGGTAGGTCTCTTTGGTAGAGGGTT	
	Y K C K V S N K A L P A P I E K T I S K -	
361	GCCAAAGGGCAGCCCCGAGAACACAGGGTGTACACCCCTGCCCCATCCCCGGATGAGCTG	420
	CGGTTCCCGTGGGGCTCTTGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGAC	
	A K G Q P R E P Q V Y T L P P S R D E L -	
421	ACCAAGAACCGGTCAAGCCTGACCTGGCTAAAGGCTTCTATCCAGGCACATCGCC	480
	TGGTTCTGGTCCAGCGGACTGGACGGACCAGTTCCGAAGATAGGGTGGCTGTAGCGGG	
	T K N Q V S L T C L V K G F Y P S D I A -	
481	GTGGAGTGGAGAGCAATGGCAGCCCCGAGAACAACTACAAAGACCAAGGCCCTCCCGTGCTG	540
	CACCTCACCCCTCTCGTTACCCGGTCCGGCCTCTGGTGTGATGTTCTGGTAGGGCACGAC	

**FIG 5A-2**

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## FIG 5B-1

V E W E S N G Q P E N N Y K T T P P V L -  
 GACTCCGACGGCTCCTTCTTACAGCAAGCTCACCGTGAGGACAAGAGGCAGGTGGCAG  
 541 ---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 600  
 CTGGGCTGCCGAGGAAGGGAGATGTCGTTGAGTGGCACCTCGTCCACCGTC

D S D G S F F L Y S K L T V D K S R W Q -  
 CAGGGAAACGTCCTCTCATGCTCCGTGATGGCATGAGGCTCTGCACAAACCAACTACAGCAG  
 601 ---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 660  
 GTCCCCCTTGAGAAGAGTACGAGGCACACTACGTA  
 GACTCCGACTACGAGGCACTACGTA  
 Q G N V F S C S V M H E A L H N H Y T Q -  
 AAGAGGCCTCTCCCTGTCTCCGGTAAGTACCGATCCAGAAAGTTCAGGACGACACAAA  
 661 ---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 720  
 TTCTCGGAGAGGGACAGAGGCCATTTCATGGCTAGGTCTTCAA  
 GCTGGCTGCTGTGGTTT

K S L S L S P G K V P I Q K V D D T K -  
 ACCTTAATTAAACGATCGTTACGGTATCACGACATCAGTCACACCCAGTCGGTGAGC  
 721 ---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 780  
 TGGAAATTAAATTGTGCTAGCAATGCGCATAGTGTGCTAGTCAGTGTGGGTCA  
 GCGCAACTCG

T L I K T I V T R I N D I S H T Q S V S -

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781 TCTAACAGAAAGTTACAGGCCCTGGACTTCATCCCGGCTCTGCACCCGATCCTGTGACCTTG  
 AGATTGTCCTCAATGTCGGACCTGAAGTAGGGCCAGACGTGGCTAGGACTGGAAC 840

S	K	Q	K	V	T	G	L	D	F	I	P	G	L	H	P	I	L	T	L	-
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

TCCAAAATGGACCAGACCCCTGGCTGTATAACCAGCAGATCTTAACCTCCATGCCGTCCCGT  
 841 AGGTTTACCTGGGTCTGGGACCATATGGTCGTCTAGAAATTGGAGGTACGGCAGGGCA 900

S	K	M	D	Q	T	L	A	V	Y	Q	Q	I	L	T	S	M	P	S	R	-
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCCGGACCTGCTGCACGTGCTGGCA  
 901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTGGAAAGCCGCTGGACGACGTGACGACCGT 960

N	V	I	Q	I	S	N	D	L	E	N	L	R	D	L	H	V	L	A	-
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

TTCTCCAATCCTGCCAACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGC  
 961 AAGAGGTTAGGACGGTGGACGGTACCCGAAGGTCCAGAACACTCTGAGACCTGAGAGACCCG 1020

F	S	K	S	C	H	L	P	W	A	S	G	L	E	T	L	D	S	L	G	-
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

GGGTCCCTGGAAAGGCTCCGGTTACAGCACCGAAGTTGCTCTGTCAGGGTCTGCAGGGT  
 1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTCAACAACGAGACAGGGCAGACGTCCCA 1080

G	V	L	E	A	S	G	Y	S	T	E	V	V	A	L	S	R	L	Q	G	-
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

**FIG 5B-2**

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## FIG 5C

TCCCTTCAGGACATGGCTTGGCAGCTGGACCTGTCTCGGGTTAATGGATCC  
1081 +-----+-----+-----+-----+-----+-----+-----+  
AGGAAGTCCTGTACGAAACCGTGCACCTGGACAGAGGCCAACAAATTACCTAGG  
- S L Q D M L W Q L D L S P G C \* -

FIG 6A-1

1 CATATGGACAAACTCACACATGCCAACCCAGCTCGGAACCTCGAAGGGTGGCCG  
 1 - +-----+-----+-----+-----+-----+-----+-----+-----+  
 61 GTATAACCTGTGTTTGAGTGTGTACGGTGGCACGGGTGAGGCTTGAGCTTCACAGGC  
 61 - +-----+-----+-----+-----+-----+-----+-----+-----+  
 M D K T H T C P P C P A P E L E G G P -  
 121 TCAGTCTTCCTCTTCCCCAAAACCCAAGGACACCCCTCATGATCTCCGGACCCCTGAG  
 121 - +-----+-----+-----+-----+-----+-----+-----+-----+  
 AGTCAGAAGGAGAAGGGGGTTTGGGTTCTGGACTAGAGGGCTGGGACTC  
 121 - +-----+-----+-----+-----+-----+-----+-----+-----+  
 S V F L F P P K P K D T L M I S R T P E -  
 181 GTCACATGGGTGGTGGAGCTGAGCCACGAAGAACCCCTGAGGTCAAGTTCAACTGGTAC  
 181 - +-----+-----+-----+-----+-----+-----+-----+-----+  
 CAGTGTACGCACCAACCCTGCACACTGGCTTCGGGACTCCAGTCAAGTTGACCATG  
 181 - +-----+-----+-----+-----+-----+-----+-----+-----+  
 V T C V V V D V S H E D P E V K F N W Y -  
 181 GTGGACGGCGTGGAGGTGCAATAATGCCAAGACAAAGCCGGAGGAGCTAACAGC  
 181 - +-----+-----+-----+-----+-----+-----+-----+-----+  
 CACCTGCCACCTCCACGTATTAACGGTTCTGTGTCATGTTGTCG  
 181 - +-----+-----+-----+-----+-----+-----+-----+-----+

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ACGTACCGTGGTCAGCGTCCTCACCGTCCCTGCACCGACTGGCTGAATGGCAAAGCT  
 241 -----+-----+-----+-----+-----+-----+-----+-----+ 300  
 TGCATGGCACACCAGTCGCAAGGAGTGGCAGGACGTGGTCTCTGACCGACTTACCGTTTCGA  
  
 T Y R V V S V L T V L H Q D W L N G K A -  
  
 TACGCATGCCGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAA  
 301 -----+-----+-----+-----+-----+-----+-----+-----+ 360  
 ATGGCTACGCCAGAGGGTCTGGTACGGGTCTGGTACGGGTCTGGTAGAGGGTT  
  
 Y A C A V S N K A L P A P I E K T I S K -  
  
 GCCAAAGGGCAGCCCCGAGAACCAACAGGTGTACACCCCTGCCCATCCGGGATGAGCTG  
 361 -----+-----+-----+-----+-----+-----+-----+-----+ 420  
 CGGTTTCCCGTCCGGCTCTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGAC  
  
 A K G Q P R E P Q V Y T L P P S R D E L -  
  
 ACCAAGAACCGGTCAAGCCTGACCTGGCTAAAGGTTCTATCCCAGGGACATCGCC  
 421 -----+-----+-----+-----+-----+-----+-----+-----+ 480  
 TGTTTCTGGTCCAGTCGGACTGGACGGACCAGTTCCGAAGATAGGGTCTGTAGGG  
  
 T K N Q V S L T C L V K G F Y P S D I A -  
  
 GTGGAGTGGAGAGCAATGGCGAGCCGGAGAACAACTACAAGACACGGCTCCCGTGCTG  
 481 -----+-----+-----+-----+-----+-----+-----+-----+ 540  
 CACCTCACCTCTGGTTACCCGTCTGGCCTCGGCTTGATGTTCTGGAGGGCACGAC

FIG 6A-2

## FIG 6B-1

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V	E	W	E	S	N	G	Q	P	E	N	N	Y	K	T	T	P	P	V	L	-
GACTCCGACGGCTCCTTCTTACAGCAAGCTCACCGTGGACAAGGCCAGGTGGCAG																				
541	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	600
CTGAGGCTGCCGAGGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTGTCCACCGTC																				
D	S	D	G	S	F	F	L	Y	S	K	L	T	V	D	K	S	R	W	Q	-
CAGGGAAACGTCTTCTCATGCTCCGTATGCCATGAGGCCCTCTGCACAAACCACTACACGCAG																				
601	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	660
GTCCCCCTTGAGAAGGACTACGGCAACTACGTAACTCCGAGACGTGGTGTGATGTGGTC																				
Q	G	N	V	F	S	C	S	V	M	H	E	A	L	H	N	H	Y	T	Q	-
AAGAGCCTTCCCTGTCTCCGGTAAAGTACCGATCCAGAAAGTTCAAGGACACACAAA																				
661	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	720
TTCTGGAGAGGGACAGAGGCCATTCACTGGCTAGGTCTTTCAAGTCCTGCTGTGGTT																				
K	S	L	S	L	S	P	G	K	V	P	I	Q	K	V	Q	D	D	T	K	-
ACCTTAATTAAACGATCGTTACGGGTATCAACGACATCAGTCACACCCAGTCGGTGAGC																				
721	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	780
TGGAAATTAAATTGGCTAGCAATGGCATAAGTTGCTGTAGTCAGTGTGGGTCAAGCCACTCG																				
T	L	I	K	T	I	V	T	R	I	N	D	I	S	H	T	Q	S	V	S	-

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TCTAAACAGAAAGTTACAGGCCCTGGACTTCATCCCCGGTCTGCACCCGATCCTGACCTTG 781   -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840 AGATTGTCTTCAATGTCCGGACCTGAAGTAGGGCCAGACGTGGCTAGGACTTGGAAC	S K Q V T G L D F I P G L H P I L T L -  TCCAATAATGGACCAGACCCCTGGCTATACCAGCAGATCTTAACCTTACCATGCCGTCCCCGT 841   -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900 AGGTTTTACCTGGTCTGGGACCGACATATGGTCCGTCTAGAAATTGGAGGTACGGCAGGGCA	S K M D Q T L A V Y Q Q I L T S M P S R -  AACGTTATCCAGATCTAACGACCTCGAGAACCTTCGGAGACCTTCGGCACGTGGCTGGCA 901   -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 960 TTGCAATAAGGTCTAGAGATTGCTGGAGCTCTGGAGCTGGAAAGGGCTGGACGACGTGCACGACCGT	N V I Q I S N D L E N L R D L L H V L A -  TTCTCCAATCCTGCCACCTGCATGGCTTCAGGTCTGGACTCTGGACCTCTGGCTGGGC 961   -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020 AAGAGGTTAGGACGGTGGACGGTACCCGAAGTCCAGAACACTCTGAGAGACCTGAGAGACCCG	F S K S C H L P W A S G L E T L D S L G -  GGGTCCTGGAAAGCATCCGGTTACAGCACCCGAAGTTGTGCTCTGTCGGGTCTGCAGGGT 1021   -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080 CCCCAGGACCTTCGTAGGCCAATGTCTGGCTCAACAAACGAGAACAGGGCAGACGTCCCA	G V L E A S G Y S T E V V A L S R L Q G -
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FIG 6B-2

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## FIG 6C

1081 TCCCTTCAGGACATGCTTGGCAGCTGGACCTGGTCTCGGGTTGTTAATGGATCC  
1135 AGGAAAGTCCTGTACGAAACCGTGCACCTGGACAGAGGCCAACATTACCTAGG

S L Q D M L W Q L D L S P G C \*

## INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 97/23183

A. CLASSIFICATION & SUBJECT MATTER  
IPC 6 C12N15/62 C07K14/575 A61K38/17

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
IPC 6 C12N C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

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1

Date of the actual completion of the international search

3 April 1998

Date of mailing of the International search report

30.04.98

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## INTERNATIONAL SEARCH REPORT

Int'l Application No  
PCT/US 97/23183

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